

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 3, 2006, 00:41:37 ; Search time 941 Seconds
(without alignments)
2899.994 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVFKNTRPKIAMVSGMI.....GSIDEVKEMQKAIALDASK 330

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| Ygapop 10.0 | Ygapext 0.5 | |
| Fgapop 6.0 | Fgapext 7.0 | |
| Delop 6.0 | Delext 7.0 | |

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DEPOP=6 -DELEXT=7

Database : Published Applications NA Main:

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| 4: | /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.* |
| 5: | /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.* |
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| 9: | /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.* |
| 10: | /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 1034.5 | 61.3 | 1785 | 3 | US-09-216-393-311 |
| 2 | 1034.5 | 61.3 | 1785 | 3 | US-09-216-393-311 |
| 3 | 1034.5 | 61.3 | 1785 | 6 | US-10-321-856-311 |
| 4 | 1034.5 | 61.3 | 1785 | 6 | US-10-321-856-311 |
| 5 | 880.5 | 52.2 | 960 | 6 | US-10-369-493-41525 |
| 6 | 873.5 | 51.7 | 957 | 6 | US-10-369-493-35128 |
| 7 | 873.5 | 51.7 | 960 | 6 | US-10-369-493-38176 |

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|------------------------|--|-----------|---------------|------|
| Alignment Scores: | | 4.91e-111 | Length: | 1785 |
| Pred. No.: | | 1034.50 | Matches: | 193 |
| Score: | | 77.3% | Conservative: | 55 |
| Percent Similarity: | | 60.1% | Mismatches: | 72 |
| Best Local Similarity: | | 61.3% | Indels: | 1 |
| Query Match: | | 3 | Gaps: | 1 |
| DB: | | | | |

ALIGNMENTS

RESULT 1

US-09-216-393-311
; Sequence 311, Application US/09216393
; Patent No. US20010014447A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, AND NUCLEIC ACID MOLECULES, AND
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216.393
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/994.825
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 311
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Toxoplasma gondii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(75)
US-09-216-393-311

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| 8 | 873.5 | 51.7 | 960 | 6 | US-10-369-493-38561 | Sequence 38561, A |
| 9 | 862.5 | 51.1 | 933 | 6 | US-10-369-493-44435 | Sequence 44435, A |
| 10 | 862.5 | 51.1 | 969 | 6 | US-10-369-493-35747 | Sequence 35747, A |
| 11 | 850.5 | 50.4 | 963 | 6 | US-10-369-493-40766 | Sequence 40766, A |
| 12 | 848.5 | 50.3 | 960 | 6 | US-10-369-493-31700 | Sequence 31700, A |
| 13 | 847.5 | 50.2 | 960 | 6 | US-10-369-493-34210 | Sequence 34210, A |
| 14 | 740 | 43.8 | 939 | 6 | US-10-369-493-46924 | Sequence 46924, A |
| 15 | 709 | 42.0 | 945 | 6 | US-10-369-493-41082 | Sequence 41082, A |
| 16 | 697 | 41.3 | 936 | 6 | US-10-369-493-40205 | Sequence 40205, A |
| 17 | 689 | 40.8 | 855 | 6 | US-10-369-493-42814 | Sequence 42814, A |
| 18 | 675.5 | 40.0 | 959 | 6 | US-10-369-493-37272 | Sequence 37272, A |
| 19 | 672 | 39.8 | 927 | 6 | US-10-369-493-32732 | Sequence 32732, A |
| 20 | 652.5 | 38.7 | 912 | 6 | US-10-369-493-34088 | Sequence 34088, A |
| 21 | 649.5 | 38.5 | 978 | 6 | US-10-369-493-41907 | Sequence 41907, A |
| 22 | 641 | 38.0 | 978 | 7 | US-10-724-972A-3485 | Sequence 3485, Ap |
| 23 | 635 | 37.6 | 912 | 6 | US-10-369-493-34859 | Sequence 34859, A |
| 24 | 635 | 37.6 | 951 | 6 | US-10-369-493-43537 | Sequence 43537, A |
| 25 | 634 | 37.6 | 975 | 6 | US-10-369-493-26509 | Sequence 26509, A |
| 26 | 628 | 37.2 | 897 | 6 | US-10-369-493-33451 | Sequence 33451, A |
| 27 | 626.5 | 37.1 | 915 | 6 | US-10-369-493-34654 | Sequence 34654, A |
| 28 | 625.5 | 37.1 | 927 | 6 | US-10-369-493-42545 | Sequence 42545, A |
| 29 | 621 | 36.8 | 822 | 3 | US-09-974-300-56 | Sequence 56, Appl |
| 30 | 605.5 | 35.9 | 1008 | 6 | US-10-369-493-23825 | Sequence 23825, A |
| 31 | 569 | 33.7 | 1005 | 6 | US-10-369-493-23812 | Sequence 23812, A |
| 32 | 560.5 | 33.2 | 942 | 6 | US-10-369-493-46543 | Sequence 46543, A |
| 33 | 518 | 30.7 | 595 | 6 | US-10-369-493-38013 | Sequence 38013, A |
| 34 | 498.5 | 29.5 | 678 | 3 | US-09-974-300-4543 | Sequence 4543, Ap |
| c 35 | 481.5 | 28.5 | 1163020 | 7 | US-10-398-221-10 | Sequence 10, Appl |
| c 36 | 478 | 28.3 | 945 | 6 | US-10-369-493-42017 | Sequence 42017, A |
| c 37 | 473.5 | 28.1 | 3011208 | 7 | US-10-398-221-2058 | Sequence 2058, Ap |
| 38 | 462 | 27.4 | 936 | 6 | US-10-369-493-40366 | Sequence 40366, A |
| 39 | 460 | 27.3 | 966 | 6 | US-10-369-493-46760 | Sequence 46760, A |
| 40 | 458 | 27.1 | 936 | 6 | US-10-369-493-40390 | Sequence 40390, A |
| 41 | 455 | 27.0 | 957 | 6 | US-10-154-460-45 | Sequence 45, Appl |
| 42 | 440.5 | 26.1 | 1062 | 3 | US-09-938-842A-1938 | Sequence 1938, Ap |
| 43 | 440.5 | 26.1 | 1062 | 3 | US-09-938-842A-1938 | Sequence 1938, Ap |
| 44 | 439.5 | 26.0 | 960 | 6 | US-10-369-493-26756 | Sequence 26756, A |
| 45 | 439 | 26.0 | 936 | 6 | US-10-369-493-40165 | Sequence 40165, A |

QY 228 ValAlaGlyGlyGluValArgLeuGluGlyGlnGlySerAlaTyrThrAlaProGly 247
 DB 769 GTGCTGGCGGAGATGTCCTCCCGCCAGGGTTCGCTTACTACGCCCCCGCC 828
 QY 248 AlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCys 267
 DB 829 GCATCGGCTGTCCGATGCGCAACATCTTCTTGAACGACGAAAGCGCTCATCCCGTGC 888
 QY 268 SerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysVal 287
 DB 889 AGTGTGTACTGCAACGAGGATGCGCTTTGAAGGACATGTTCAATTGGTCTCCCGCGCTC 948
 QY 288 IleGlyGlyArgGlyValGluLysIleIleGluLeuGluThrAlaGlnGluArgGln 307
 DB 949 ATGGAGGCGCGGATCGATCGCGCTCATCGAGCTCGAGCTGAACGAGGAGGAGAGAG 1008
 QY 308 GluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAsp 327
 DB 1009 CAGTTCCAGAGTCCGTCGACGAGCTCATGGCGCTCAACAGGCGGTGCTCTTCAG 1068
 QY 328 Ala 328
 DB 1069 GCG 1071

RESULT 3
 US-10-321-856-311
 ; Sequence 311, Application US/10321856
 ; Publication No. US20030194393A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Milhausen, Michael James
 ; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: TX-1-C2-1
 ; CURRENT APPLICATION NUMBER: US/10/321,856
 ; CURRENT FILING DATE: 2002-12-17
 ; PRIOR APPLICATION NUMBER: 09/216,393
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 08/994,825
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 366
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 311
 ; LENGTH: 1785
 ; TYPE: DNA
 ; ORGANISM: Toxoplasma gondii
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(75)
 ; OTHER INFORMATION:
 US-10-321-856-311

Alignment Scores:
 Pred. No.: 4,91e-111 Length: 1785
 Score: 1034.50 Matches: 193
 Percent Similarity: 77.3% Conservative: 55
 Best Local Similarity: 60.1% Mismatches: 72
 Query Match: 61.3% Indels: 1
 DB: 6 Gaps: 1

US-09-390-846-2 (1-330) x US-10-321-856-311 (1-1785)

QY 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
 DB 109 AGAAAGAGGTGGCCATGATGGCTCTGCGATGATTGGTGGCACTATGGCTACCTGTGC 168
 QY 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValProAsnMetProMetGly 48
 DB 169 GCTCTCCGTGAGCTCGCTGACGCTGCTCTTACAGATGTTGTCAGAGGTATGCCGAGGT 228
 QY 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
 DB 229 AAGGCTCTTGACCTGAGCCATGTGACCTCCGCTGCTGACACCAACAGTTTCGCTCGCTCT 288
 QY 69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleIleThrAlaGlyIle 87

DB 289 GAGTACTCTTACGAGCGCGCTCACCAGTCCGAGTCCGTTATCGTTATCCCGCGCTCG 348
 QY 88 ThrLysIleProGlyLysSerAspLysGluTyrPsrArgMetAspLeuLeuProValAsn 107
 DB 349 ACCAAGGTGCGCGGCAAGCCGACTCCGAGTGGAGCCGAAACGATCTGCTCCCGTTCAAC 408
 QY 108 IleLysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheVal 127
 DB 409 TCGAAGATCATCTCGCGAGATCGTTCAGAACATCAAGAAAGTACTGCCCAAGACCTTCATC 468
 QY 128 IleAsnIleThrAspProLeuAspValMetValAlaIleLysGlnSerSerGlyLeu 147
 DB 469 ATCTGGTGCACCAACCCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 528
 QY 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
 DB 529 CGGACCAACATCATCTCGCGTATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 QY 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
 DB 589 GTGCGGAGCGGCTGCTGCTCTCTCCCGCGAGCTCCAGGCCACCGTTCATCGGCACACAC 648
 QY 188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu 207
 DB 649 GCGGACTCATGCTGCTCCGCTTGTCCGCTTACATACCGTGAACGACTACCCGATCCAGAAG 708
 QY 208 PheValLysLysGlyTyrIleLysGlnGluValAspAspIleValGlnLysThrLys 227
 DB 709 TTCATCAGGAGCGGCTAGTCCGAGAGGAGCTCCGAGGAGATCGCTGAGCAGACACCAAA 768
 QY 228 ValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrThrAlaProGly 247
 DB 769 GTGCTGGCGCGAGATCGTCCGCTTCTCCGCGAGGCTTCGCTTACTAGCGCCCGCC 828
 QY 248 AlaSerAlaIleGlnMetAlaGluSerTyrLysLysAspArgLysArgValMetValCys 267
 DB 829 GCATCCGCTGTCCGCTTCCGCTTCTTGAACGACGAAAGCGGCTCATCCCGCTGC 888
 QY 268 SerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysVal 287
 DB 889 AGTGTGTACTGCAACGAGGAGTACGCTTGAAGGACATGTTCAATTGGTCTCCCGCGCTC 948
 QY 288 IleGlyGlyArgGlyValGluLysIleIleGluLeuGluThrAlaGlnGluArgGln 307
 DB 949 ATGGAGGCGCGGATCGATCGCGCTCATCGAGCTCGAGCTGAACGAGGAGGAGAGAG 1008
 QY 308 GluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAsp 327
 DB 1009 CAGTTCCAGAGTCCGTCGACGAGCTCATGGCGCTCAACAGGCGGTGCTCTTCAG 1068

QY 328 Ala 328
 DB 1069 GCG 1071

RESULT 4
 US-10-321-856-313
 ; Sequence 313, Application US/10321856
 ; Publication No. US20030194393A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Milhausen, Michael James
 ; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: TX-1-C2-1
 ; CURRENT APPLICATION NUMBER: US/10/321,856
 ; CURRENT FILING DATE: 2002-12-17
 ; PRIOR APPLICATION NUMBER: 09/216,393
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 08/994,825
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 366
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 313
 ; LENGTH: 1785

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; TYPE: DNA
; ORGANISM: Toxoplasma gondii
US-10-321-856-313

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  4.91e-111      Length: 1785
Pred. No.:      1034.50      Matches: 193
Score:          77.3%      Conservative: 55
Percent Similarity:
Best Local Similarity: 60.1%      Mismatches: 72
Query Match:      61.3%      Indels: 1
DB:              6          Gaps: 1

US-09-390-846-2 (1-330) x US-10-321-856-313 (1-1785)

Qy 9 ArgProlylAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 109 AGAAGAAGGTGGCCATGATTGGCTCTGGCATGATTGGTGCCACTATGGGTCTACCTGTGC 168
Qy 29 SerLeuArgGluLeuGlyAspValValPheAspValValProAsnMetProMetGly 48
Db 169 GCTCTCCGTGAGCTGCGTGGCTGCTTCTCTACGATGTTGTCAAGAGGTATGCCCGAGGGT 228
Qy 49 LysAlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrValTyrgly 68
Db 229 AAGGCTCTTGACCTGAGCCATGTGACCTCCGTTGGTTCGACACCAACGTTTCGTCGGTCT 288
Qy 69 SerAsnSerTyrglu--CysLeuLysGlyAlaAspValValIleIleThrAlaGlyIle 87
Db 299 GAGTACTCTACGAGCGCGCTCACCGTGGGACTCGGTATTCGTTACCGCGGTCTG 348
Qy 88 ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuProValAsn 107
Db 349 ACCAAGGTGCGGGCAAGCCGACTCCGAGTGGAGCCGAAACGATCTCTCCCGTCAAC 408
Qy 108 IleLysIleMetArgGluValGlyAlaIleLysSerTyrglyPheAsnAlaPheVal 127
Db 409 TCGAAGATCATTCGGGAGATCGGTGAGAACATCAAGAGTACTGCCCCAAACCTTTCATC 468
Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaLeuLeuGlnGluSerSerGlyLeu 147
Db 469 ATCGTGGTCAACCAACCCGCTGAGTGCATGTCGAGGTCAATGCGGAGCGCTTCGGCTC 528
Qy 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
Db 529 CCGACCAACATGATTCGGGTATGCGCTGCAATGCTCGACTCTGCTGCTTCGCGCATAC 588
Qy 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
Db 589 GTGCGGACGCGCTGTCTCTCCCGGACGTCGAGTCCAGGCCACCGTTCATCGGCACACAC 648
Qy 188 GlyAspHisMetValProLeuSerArgTyrglyAlaThrValAsnGlyIleProLeuSerGlu 207
Db 649 GCGCATGATGTCGCGTTCGCGTACATTCGCTGAAACGACTACCGCATCCGAGTCCAGAAG 708
Qy 208 PheValLysLysGlyTrpIleLysGlnGluValAspAspIleValGlnLysThrLys 227
Db 709 TTTCATCAAGACGCGGTAGTACCGAGAGAGCAGCTCGAGGAGATCGCTGAGCACACCAAA 768
Qy 228 ValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrglyAlaProGly 247
Db 769 GTGCTGCGCGGAGATCGCTGCTTCCTCGGCCAGGGTTCGCTTACTACGCCCCCGCC 828
Qy 248 AlaSerAlaIleGlnMetAlaGluSerTyrglyLeuLysAspArgLysArgValMetValCys 267
Db 829 GCATCGCTGTCCCATGCAACATCTTCTTGAACGACGAAAGCGGTCTATCCCGTGC 888
Qy 268 SerCysTyrglyGlnGlyGlnTyrglyValGlnAsnHisTyrglyLeuGlyValProCysVal 287
Db 889 AGTGTTACTGCAACCGGAGATGACGCTTGAAGGACATGTTCAATTGGTCTCCCGCGCTC 948
Qy 288 IleGlyGlyArgGlyValGlyLysIleLeuGluLeuLeuThrAlaGlnGluArgGln 307
Db 949 ATTGAGGCGCGGCATCGAGCGCGTTCATCGAGCTCGAGCTGAACGAGGAGGAGAGAG 1008
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Qy 308 GluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAsp 327
Db 1009 CAGTTCCAGAAAGTCCGTCGACGACGTCATGCGCGCTCAACAGCGGTTCCTCTTCAG 1068
Qy 328 Ala 328
Db 1069 GCG 1071

RESULT 5
US-10-369-493-41525
; Sequence 41525, Application US/10369493
; Publication No, US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 41525
; LENGTH: 960
; TYPE: DNA
; ORGANISM: SPHINGOMONAS
US-10-369-493-41525
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Alignment Scores:
Pred. No.:      2.88e-93      Length: 960
Score:          880.50      Matches: 173
Percent Similarity: 70.7%      Conservative: 54
Best Local Similarity: 53.9%      Mismatches: 89
Query Match:      52.2%      Indels: 1
DB:              6          Gaps: 1
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US-09-390-846-2 (1-330) x US-10-369-493-41525 (1-960)

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Db 7 CGCAAGAAGATCGCGCTCGATCGGCTCCGGCATGATCGGTGGCACCTTCGCGACCTTCGCT 66
Qy 29 SerLeuArgGluLeuGlyAspValValPheAspValValProAsnMetProMetGly 48
Db 67 GCATCAAGNACTGGGCGATATGCTCTGTCACATTCGCGAGGGGACCGCGCAGGCG 126
Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrgly 68
Db 127 AAGCGCTCGACATCGCACAGTCCGACCGGTCCGAAGCGTTCGATGCCAACCTCAAGGCG 186
Qy 69 SerAsnSerTyrglyCysLeuLysGlyAlaAspValIleIleThrAlaGlyIleThr 88
Db 187 CGCAACAGTACGAGGACATTCGCGGCGCGCCACGCTGCTCATCCGCGGTATCCCG 246
Qy 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
Db 247 CGCAAGCGGGC-----ATGAGCGCGGACGATCTTCTCAAGACCAACCTG 291
Qy 109 LysIleMetArgGluValGlyAlaIleLysSerTyrglyCysProAsnAlaPheValIle 128
Db 292 GCGGTGATGAAGCGGTGGGCGAGGGCATCGCGGACCGCGCGCGCGCGCGGTTCGTGATC 351
Qy 129 AsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeuPro 148
Db 352 TGCATCAACCAACCGCGCTCGACGCGATGTTGGGGCGCTGCGCGAGTTCGCGCGCTCGCG 411
Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
Db 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
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Db 412 CACGAGAGGTCTCGGCATGCGCGGCTCGACTCGCGCGCTTCGCCACTTCCTC 471
 Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
 Db 472 GCCGAGGATTCACAGTCTCGGTCGAGGACGTCACCGCTTCGTCGTCGCGGACACGCGC 531
 Qy 169 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyLeuProLeuSerGluPhe 208
 Db 532 GACACCATGTCCTCGGTGATCGAGTATTCGACGTCGCGGCGCATCCCGTGCCGACCTG 591
 Qy 209 ValLysLysGlyTyrIleLysGlnGluValAspAspIleValGlnLysThrLysVal 228
 Db 592 ATCAAGATGGGTGTCTCCACCGAGCGCATCGAGCCATCGTCGCGGACCGCGCTCG 651
 Qy 229 AlaGlyGlyIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
 Db 652 GCGCGCGCGAGATCGTCGCTGCTCAAGACCGCTCGGCTATTCGCGCGCGCCACC 711
 Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
 Db 712 AGCGCATCGCATGCGCGAGAGCTATCTGAAGGACAAAGACGCGCTCTCCCTGTGCC 771
 Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
 Db 772 GCGCACTTACCGCGCAGTACGCGCTCGACGATCTGTACGTCGCGGCTGCGGATCGTATC 831
 Qy 289 GlyArgGlyValGluLysIleLeuLeuGluLeuThrAlaGlnGluArgGlnGlu 308
 Db 832 GCGAGGACGCGCTCGAGCGCATCGTCGAGATCGAGCTGAACGCCACGCGGAGCAGAT 891
 Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAspAla 328
 Db 892 TTCGACGCTCGTGTGTCGCTCAAGAACTGTCGAGCATGCAAGTCGATCGACGCC 951
 Qy 329 Ser 329
 Db 952 TCG 954

RESULT 6

US-10-369-493-35128
 ; Sequence 35128, Application US/10369493
 ; Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 35128
 LENGTH: 957
 TYPE: DNA
 ORGANISM: Agrobacterium tumefaciens

US-10-369-493-35128

Alignment Scores:
 Pred. No.: 1,92e-92 Length: 957
 Score: 873.50 Matches: 167
 Percent Similarity: 72.3% Conservative: 60
 Best Local Similarity: 53.2% Mismatches: 82
 Query Match: 51.7% Indels: 5
 Gaps: 1

US-09-390-846-2 (1-330) x US-10-369-493-35128 (1-957)

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28

Db 7 CGCAAAAAATTCGCACTTATTGGTTCTGGCATGATCGCGGCACGCTCGCGCATTCGCC 66
 Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
 Db 67 AGCTCTGAGGAACATGGCGGATATCGTCTCTTCGACATCGCGGCGCATCCCGGAGGC 126
 Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
 Db 127 AAGGTCGTGATATTGCCAGTCGCGCGCGGTGAAGGCTTCAATGCAAGAGCTCTCCGC 186
 Qy 69 SerAsnSerTyrGluCysLeuLysGlyAlaAspValIleIleThrAlaGlyIleThr 88
 Db 187 GCTTCGATACGCGCGCATGAAGGCGCACGCTCTGCATCGTCACCGAGGTTCGCC 246
 Qy 89 LysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsnIle 108
 Db 247 CGCAAGCCCGC-----ATGAGCCGCGATGATCTTCTTGGCATCAACCTC 291
 Qy 109 LysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheValIle 128
 Db 292 AAGTCTATGGAACAGTCCGCGCGCATCAAGAAATATGCTCCGACGCTTTCGTGATC 351
 Qy 129 AsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeuPro 148
 Db 352 TGCATCAACCAACCCGCTCGACGCCATGCTCTGGCGCTGCGAAGTCTTCCGCGCTCGCG 411
 Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMetIle 168
 Db 412 AAGAACAGGTCTCGCGCATGCTGGCGCTTCTCGACGCGCAGCTTCCGCTGTCTCT 471
 Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
 Db 472 GCCGAAGAATTCAGGTTTCGTCGCGACGCTCACCGCTTCGTTCTCGCGGTTCATGCG 531
 Qy 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe 208
 Db 532 GACACCATGTCGCGCTCGCGCTTATTCACCGCTTGGCGGCTTCCGCTTACCGATCTC 591
 Qy 209 ValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLysVal 228
 Db 592 GTCAAGATGGCTGTGTGACCGCGAAGCTTTCGACGAGATCATCCGCGCACCGGTGAC 651
 Qy 229 AlaGlyGlyIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
 Db 652 GCGCGCGGGAATCGTCGCGCTCTTGAAGACCGGCTCGGCTATTACGCGCGCGCGCT 711
 Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
 Db 712 TCGGCTATCGAAATGCGCGAATCTTACCTCAAGGACAAAGACGCGTCTCGCGCTGCT 771
 Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
 Db 772 GCCACCTTTCGCGCGCAGTATGCGGTAGACCATGATATGTCGCGCTGCCCATCATC 831
 Qy 289 GlyArgGlyValGluLysIleLeuLeuGluLeuThrAlaGlnGluArgGlnGlu 308
 Db 832 GTTCCGCGGTATCGAGCGGTATCGAGATCGAATGAACTGAACAGGAGAAAGAGAGCCGCC 891
 Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAla 322
 Db 892 TTCCAGAAATCCGTCGCGCTGCTCGCTGCTTCTTTCGGAAGCC 933

RESULT 7

US-10-369-493-38176
 ; Sequence 38176, Application US/10369493
 ; Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38176
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38176

Alignment Scores:
Pred. No.: 1,93e-92 Length: 960
Score: 873.50 Matches: 167
Percent Similarity: 72.3% Conservative: 60
Best Local Similarity: 53.2% Mismatches: 82
Query Match: 51.7% Indels: 5
DB: 6 Gaps: 1

US-09-390-846-2 (1-330) x US-10-369-493-38176 (1-960)

QY 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
DB 7 CGCAAAAAATTCGCTATTGGTCTGGCATGTCGGCGCACGCTGGCGCATCTCGCC 66
QY 29 SerLeuArgGluLeuGlyValValLeuPheAspValProMetGly 48
DB 67 AGCTTGAAGAACTGGCGGATATCTCTTCGACATCGCGACGGATCCCGCAGGCG 126
QY 49 LysAlaMetAspIleSerHisSerValValAspThrGlyIleThrValTyrGly 68
DB 127 AAGGTCTGGATATTGCCAGTCCGCGCGGTGAAGGCTTCAATGCAAAAGCTCTCGCG 186
QY 69 SerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleThrAlaGlyIleThr 88
DB 187 GCTTCGGATTACCGCGCCATCAAGGCGCAGACGTCGTCATGTCACGCGAGTGTGCC 246
QY 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
DB 247 CCAGACCCCGC-----ATGACCCGGATGATCTTTCGGCATCAACCTC 291
QY 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValIle 128
DB 292 AAGGTCAATGAAGTCCGCGCGCATCAAGAAATATGCTCCGAACGCTTTCGTGATC 351
QY 129 AsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro 148
DB 352 TGCATCACCACACCGCTCGACGCCATGGTCTGGGCGCTGCAAGATCTTCCGGCGTGGCG 411
QY 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
DB 412 AAGAACAGGTCTGGCATGCTGGCGTCTCGACAGCGACGCTTCCGCCCTGTTCCT 471
QY 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
DB 472 CGCGAAGATTCACGTTTCGGTCCAGGACGTCACCGCTTCTGTCGCGGTTCATGCG 531
QY 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe 208
DB 532 GACACCATGTCGCGCTCGCGTTATTCACCGTTGGCGGCTTCCGCTTACCGCATCTC 591
QY 209 ValLysLysGlyTrpIleLysGlnGluValAspAspIleValGlnLysThrLysVal 228
DB 592 GTCAAGATCGGCTGGTTGACCCCGAACGCTCTTGACAGCATCATCCAGCGCACCGGTGAC 651
QY 229 AlaGlyGlyLeuValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
DB 652 GCGCGCGGAAATCGTCGCGCTTTGAAGACCGGCTCGGCTTATTACGCGCGCGCGCT 711
QY 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268

DB 712 TCGGCTATCGAAATGGCGAATCTACTCTCAAGACAAAGAGCGGTTCTGCCCGCTGCT 771
QY 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
DB 772 GCCCACCTTTTCGGGCCAGTATGGCGTAGACACATATGTATGTGGCGGTGCCCATCATC 831
QY 289 GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308
DB 832 GGTCCGCGCGGTATCGAGCGCGTCTAGATGAATGAACAAGAGAAAGAACGCCGCC 891
QY 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAla 322
DB 892 TTCCAGAAATCCGTCGGCGCTGCTCGCTGGTCTTTTCGGAAGCC 933

RESULT 8

US-10-369-493-38561
; Sequence 38561, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 38561

; LENGTH: 960

; TYPE: DNA

; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-38561

Alignment Scores:

Pred. No.: 1,93e-92 Length: 960
Score: 873.50 Matches: 167
Percent Similarity: 72.3% Conservative: 60
Best Local Similarity: 53.2% Mismatches: 82
Query Match: 51.7% Indels: 5
DB: 6 Gaps: 1

US-09-390-846-2 (1-330) x US-10-369-493-38561 (1-960)

QY 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
DB 7 CGCAAAAAATTCGCTATTGGTCTGGCATGTCGGCGCACGCTGGCGCATCTCGCC 66
QY 29 SerLeuArgGluLeuGlyValValLeuPheAspValProMetGly 48
DB 67 AGCTTGAAGAACTGGCGGATATCTCTTCGACATCGCGACGGATCCCGCAGGCG 126
QY 49 LysAlaMetAspIleSerHisSerValValAspThrGlyIleThrValTyrGly 68
DB 127 AAGGTCTGGATATTGCCAGTCCGCGCGGTGAAGGCTTCAATGCAAAAGCTCTCGCG 186
QY 69 SerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleThrAlaGlyIleThr 88
DB 187 GCTTCGGATTACCGCGCCATCAAGGCGCAGACGTCGTCATGTCACGCGAGTGTGCC 246
QY 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
DB 247 CCAGACCCCGC-----ATGACCCGGATGATCTTTCGGCATCAACCTC 291
QY 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValIle 128
DB 292 AAGGTCAATGAAGTCCGCGCGCATCAAGAAATATGCTCCGAACGCTTTCGTGATC 351

| | | | |
|----|-----|--|-----|
| Qy | 129 | AsnIleThrAsnProLeuAaspValMetValAlaLeuGlnGluSerSerGlyLeuPro | 148 |
| Dd | 352 | TGCATCACCAACCCCTCGACGCCATTGGTCTCGGGCGCTGCAGAAATTCTCCGGCCTCGCG | 411 |
| Qy | 149 | HisHisArgIleCysGlyMetAlaGlyMetLeuAaspSerSerArgPheargMettile | 168 |
| Dd | 412 | AAGAACAAGGTCTCGGCATGGCTGGGTTCGACAGCGCAGCTTC CGCCTGTTCCT | 471 |
| Qy | 169 | AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly | 188 |
| Dd | 472 | GCCGAAGAATTCAACGTTTCGTC CAGGACGTCACCGCCTTCGTTCTCGCGCGTCATGCG | 531 |
| Qy | 189 | AspHisMetValProLeuSerSerArgTyrrAlaThrValAsnGlyIleProLeuSerGluPhe | 208 |
| Dd | 532 | GACACCATTGGTGGCGCTCGCCGTTATTCCACCGTTGGCGGCTTCGCTTACCATCTC | 591 |
| Qy | 209 | ValLysLysGlyTrpIleLysGlnGluValAaspAprIleValGlnLysThrLysVal | 228 |
| Dd | 592 | GTC AAGATGGCTGGTGACCGCCGACGCTCTTGAGCAGATCATCAGCGCACCCGCTGAC | 651 |
| Qy | 229 | AlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrrAlaProGlyAla | 248 |
| Dd | 652 | GGCGCGCGGAAATCTCGGCCTCTTTGAAGACCGGCTCGGCCATTACGGCGCGCCGCT | 711 |
| Qy | 249 | SerAlaIleGlnMetAlaGluSerTyrrLeuLysAaspArgLysArgValMetValCysSer | 268 |
| Dd | 712 | TCGGCTATCGAAATGGCCGAATCTCTACCTCAAGGACAAGAAGCGGTTTCGCGCGCTGT | 771 |
| Qy | 269 | CysTyrrLeuGlnGlyGlnTyrrGlyValGlnAsnHisTyrrLeuGlyValProCysValIle | 288 |
| Dd | 772 | GCCCACCTTTCCGGCCAGTATGGGTAGACGACATGTATGTCCGGGTGCGCCACCATCATC | 831 |
| Qy | 289 | GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnIleArgGlnGlu | 308 |
| Dd | 832 | GGTCCGCGCGTATCGACGCGCTCATCGAGATCGAACTGACACAAGGAAGAAGACCGCC | 891 |
| Qy | 309 | LeuGlnGlySerIleAaspGluValLysGluMetGlnLysAla | 322 |
| Dd | 892 | TTCCAGAAATCCGTGGCGGCTGTGCTGCTGTCTTTCGGAAGCC | 933 |

RESULT 9

US-10-369-493-44435
 ; Sequence 44435, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 44435
 ; LENGTH: 933
 ; TYPE: DNA
 ; ORGANISM: Rhodospseudomonas palustris
 US-10-369-493-44435

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Alignment Scores:
Pred. No.: 3.67e-91
Score: 862.50
Length: 933
Matches: 169
Conservative: 59
Percent Similarity: 72.6%
Best Local Similarity: 53.8%
Indels: 5
Query Match: 51.1%
Gaps: 1
DB: 6
US-09-390-846-2 (1-330) x US-10-369-493-44435 (1-933)

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Db 247 CGAAGCCGGG-----ATGAGCCGCGAGCACTCTGGGCATCAACCTG 291
Qy 109 LysileMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValle 128
Db 292 AAGGTCATGAAGCGCGCGGCGAAGCATCAAGGCTCAAGCCGCCCAAGCCCTTCGTATC 351
Qy 129 AsnileThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro 148
Db 352 TGCATCACCAACCCGCTGACCGCATGGTCTGGGCCCTGACGAGATTCTCGGGCCCTGGCG 411
Qy 149 HisHisArgGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetile 168
Db 412 AAGGAAAGGTCATCGCATGCGCGCTCTCGACTCGGCCGCTTCGCTACTCTCTG 471
Qy 169 AlaPheLysLeuGluValSerProArgPheValGlnGlyMetValleGlyValHisGly 188
Db 472 GCTGAAGCACCGCGGCTCTCGGTGAAGACATCCACGCTGACCCCTGGCGGCCACGCG 531
Qy 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyLeuProLeuSerGluPhe 208
Db 532 GACGACATGGTGGCATGGTCTGCTCAGTCCGCGGCTCGCGGCTCGCCCTGCGGAATG 591
Qy 209 ValLysLysGlyTyrPileLysGlnGluValAspAspPheValGlnLysThrLysVal 228
Db 592 GTCAAGCAAGGCTGCTGCTCGCAGACAAAGCTGGAGCGCATCTGTCAGCGGCACCGCAAG 651
Qy 229 AlaGlyGlyGluLeuValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
Db 652 GCGCGCGCGAGATCGTCCCTCTGGAAGACCGGCTCGGCTCTACGCGCCCGCGAG 711
Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
Db 712 AGCGCGATCGCATGCGGCACTCTGCTGACCTGAGGACAAAGACGCGCTCTCGCGCGCC 771
Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValle 288
Db 772 ACCTACCTGCGCGCATAGCGCTGACGACCTCTATGTCGGCGCTCGCGGTGCTATC 831
Qy 289 GlyGlyArgGlyValGlyLysLeuLeuGluLeuThrAlaGlnGluArgGlnGlu 308
Db 832 GCGCGCGCGCGCGGAGAGATCGTCGATTCGAAACCAACGACGACGAGAGCGGATG 891
Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAspAla 328
Db 892 TTCGCCAAGTCGGTTCGATCGGTGAAGGCGCTGATGAAGGCTTCAAGGCCATCGACAGC 951
Qy 329 Ser 329
Db 952 TCG 954

RESULT 12

US-10-369-493-31700
; Sequence 31700, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 31700
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-31700

Alignment Scores:
Pred. No.: 1.71e-89 Length: 960
Score: 848.50 Matches: 163
Percent Similarity: 70.7% Conservative: 64
Best Local Similarity: 50.8% Mismatches: 89
Query Match: 50.3% Indels: 5
Db: 6 Gaps: 1

US-09-390-846-2 (1-330) x US-10-369-493-31700 (1-960)

Qy 9 ArgProLysIleAlaMetValGlySerClyMetileGlyGlyThrMetAlaPheLeuCys 28
Db 7 AGACCCAAAGATGCGGTGCGGGCGAGATCGCGCGCACCTCGCCCATCTCGCC 66
Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValProAsnMetProMetGly 48
Db 67 GCGATCAAGGAATGCGGAGCTGCTCTGTCGACATCGCGAAGGACCCCTCAGGGC 126
Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
Db 127 AAGGCTCTGGACATCGGCAATCGGCGCCCTCGGAAGGCTTCGACGCGCTGATGAAGGC 186
Qy 69 SerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr 88
Db 187 GCGAACAGCTACGAAGAGATCGCGGCGCGACGCTCTGCAATCGTACCGCGCGGTGCGC 246
Qy 89 LysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsnIle 108
Db 247 CGCAAGCCCGC-----ATGAGCCGCGAGCACTGATCGGCATCAACCTC 291
Qy 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValle 128
Db 292 AAGGTGATGAATCGGTCGCGAGGCGATCAAGCCCATCGCGCGCGCTTCGTGATC 351
Qy 129 AsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro 148
Db 352 TGCATCAACCAACCGCTCGACCGCATGGTCTGGCGCTGTCGACGCGCGCTTCGCGGCTGCGC 411
Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetile 168
Db 412 GCGAAGAGGTGGTGGCGATGCGCGGCGTCTGCTCGCTCGCGCGCTTCGCGCATTCCTG 471
Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValleGlyValHisGly 188
Db 472 TCGTTCGAGTTCACAGCTCTGATCGCGCGAGCTGTCGCTCGCGCGCTTCGCGCATTCCTG 531
Qy 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe 208
Db 532 GACACGATGGTGGCGCTCTGCTCGCTACTCGACGATGCGCGCATCCGCGCTCGCGATCTC 591
Qy 209 ValLysLysGlyTyrPileLysGlnGluValAspPheValGlnLysThrLysVal 228
Db 592 GTGCGATGGCTGGACCGACGAGAGATCGACAGATCGTGCGAGCGCGCCCGGTGAC 651
Qy 229 AlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
Db 652 GCGCGCCCGAGATCGTGGGCGCTCTGTAAGACCGCTCGGCTTCAGCGCGCGCCACCC 711
Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
Db 712 TCGGCCATCGAGATGGCGAAGCCTATCTCAAGACCAAGACGCTCTGCTCGCTCGCGCG 771
Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValle 288
Db 772 GCCTATGTGACGCGCGCTTCGCGCTGAAAGGATGATGTGCGGCGTTCGCGCATCATC 831
Qy 289 GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308
Db 832 GCGCGCGCGGATCGAGAGATCGTGCATCATCAAGCTCAACGACGACGAGCGCGCATG 891
Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAspAla 328

Db 892 TTCACAAAGTCGGTCAATCGGTCGAGGGCCTCGTCGAGGGCTCGAAGGGCATCGACTCC 951
Qy 329 Ser 329
|||
Db 952 TCG 954

RESULT 13
US-10-369-493-34210
; Sequence 34210, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 34210
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Sphingomonas aromaticivorans
US-10-369-493-34210

Alignment Scores:
Pred. No.: 2,24e-89 Length: 960
Score: 847.50 Matches: 167
Percent Similarity: 71.0% Conservative: 61
Best Local Similarity: 52.0% Mismatches: 88
Query Match: 50.2% Indels: 5
Gaps: 1

US-09-390-846-2 (1-330) x US-10-369-493-34210 (1-960)

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 7 CGCAAGAAGATCGCTGATCGCGCGGCAACATCGGTGGACATCTTGGCCACCTCGCC 66

Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
Db 67 GCCAGAAAGAACTTTGGCGACATCTCTCTTCGACGTCGTTGAAGGCGTGCCTCCAGGCG 126

Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
Db 127 AAGCGCTCGACCTTTTCGAGTCGCGTCCGGTCGAGGCTTCGACGCCCAACATCATCGCC 186

Qy 69 SerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleThrAlaGlyIleThr 88
Db 187 ACCACGACTACAAGGGATCCGACGGCGGACGTCATCATCTGTCACCGCGGCTCGCC 246

Qy 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
Db 247 CGCAAGCCGGC-----ATGAGCCGCGACGACCTGCTCGGCATCAACCTC 291

Qy 109 LysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheValIle 128
Db 292 AAGGTGATGAAGCCGCTCGCGAAGGATCCGCGAACACCGCGCGGTCGTGTGATC 351

Qy 129 AsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeuPro 148
Db 352 TCATCACCACCCGCTGACCGCATGTCTGGGCGCTGGCGAGTTCTCGGCGCTCGCC 411

Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
Db 412 GCGAACAAAGTCTCGGCATGCCGCGGCTCGACTCGGCGGCTTCAGCACGTTCTCTG 471

Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188

Db 472 GCATGGGAATTCGGGCTCTCGATCCGCGACGTGAACACAGTTCGTCTCGGCGGCCACGGC 531
Qy 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe 208
Db 532 GACACCATGTTTCGGTCAACCGATCTCGACCGTCAACCGCATCCCGGTGCCCGCCTC 591

Qy 209 ValLysLysGlyTrpIleLysGlnGluValAspAspIleValGlnLysThrLysVal 228
Db 592 GTCAAGATGGGCTGTCCACCCAGGAAAGATCGACGCGATCGTCAGCGCACCGCTCG 651

Qy 229 AlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
Db 652 GCGCGCGCGGATCGTCGGCTGCTCAAGACCGGTTCCGGCTTCTACGCGCTCGCGCA 711

Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
Db 712 TCGGGCATCGGATGGCGAAGCTATCTCAACGACCAAGCGCATCTCTCGGCTCGGCC 771

Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
Db 772 GCCTACGTTGACGCGGAATACGGGTGAACGGTCTTTACGTCGGCGTCCGGTCTGATC 831

Qy 289 GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308
Db 832 GCGCGAAACGCGTCGAGAAGTGATCGAGATCGAATCTCGACGACGAAGCAAGGCAAC 891

Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAspAla 328
Db 892 CTCAGGTCCTCGTCGAGCGGTCAGGAACTGCTGGAAGCCTCGAAGGGCATCGACCC 951

Qy 329 Ser 329
|||
Db 952 AGC 954

RESULT 14
US-10-369-493-46924
; Sequence 46924, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46924
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-10-369-493-46924

Alignment Scores:
Pred. No.: 1.03e-76 Length: 939
Score: 740.00 Matches: 147
Percent Similarity: 65.8% Conservative: 63
Best Local Similarity: 45.9% Mismatches: 98
Query Match: 43.8% Indels: 12
Gaps: 3

US-09-390-846-2 (1-330) x US-10-369-493-46924 (1-939)

Qy 7 AsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPhe 26
Db 7 AATACCTGTAAGAAAGTTCTGTTATCGGAGCAGGTTTACCGGAGCTACCACTCATTT 66

```

QY 27 LeuCySerLeuArgGluLeuGlyAspValValLeuPheAspVal-----ValProAsn 44
Db 67 TTAATCGCTCAAAAGAGCTGGCAGACGTTGTTCTTGTGACATTCGCGAAATTTGGAGAAC 126
QY 45 MetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIle 64
Db 127 CCGACAAAGGAAAGCGCTTGATATGCTTTGAAGCAAGCCGGTTCAAGGCTTTGACGCA 186
QY 65 ThrValTyGlySerAsnSerTyGluCysLeuLysGlyAlaAspValValIleThr 84
Db 187 AAATATTACGGGAACATCCAAATTACGAGGATACAGCCGGCTCTGACATTTGTCATTACA 246
QY 85 AlaGlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeu 104
Db 247 GCGGGTATCGCAAAACCTGGT-----ATGAGCAGAGATGATCTGGTC 291
QY 105 ProValAsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyCysProAsn 124
Db 292 TCTACAAACGAAAGATTATGAGAGCGTTACCGAGGAATCTGGAATATTCTCTGTAC 351
QY 125 AlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSer 144
Db 352 TCTATTATTGTGCTGCAAAATCTGTTGATGCAATACATACCGCGTGTACAAAGAA 411
QY 145 SerGlyLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPhe 164
Db 412 TCAGGCTTCCTTAAAGAGCGTGTAAATCGGCCAGTTCAGGTGTGCTGATACGCGAGATT 471
QY 165 ArgArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIle 184
Db 472 AGACATTGTGGCAGAGAAATTAACCTGTCTGTAAGAGATGTGATGTTGCTGACTC 531
QY 185 GlyValHisGlyAspHisMetValProLeuSerArgTyAlaThrValAsnGlyIlePro 204
Db 532 GCGGACACGGTGACGATATGTTCCGCTTGTGCGTTATCTTATGCTGCGGTATCCCG 591
QY 205 LeuSerGluPheValLysLysGlyTrpIleLysGlnGluValAspAspIleValGln 224
Db 592 CTTGAACTCTTATCCGAAA-----GAAAGGATTGACCAATTTGTTGGAG 636
QY 225 LysThrLysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyTrp 244
Db 637 CGCACTAGAAAGCGGCGGAAATCGTGAATCTTCTTGGAAACGGAAGCCGCTATTAT 696
QY 245 AlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyLeuLysAspArgLysArgVal 264
Db 697 GCGCTGCGGCTTCTCTGACAGAAATGTCGAAGCGATCTTGAAGATCAGCGCGGCTC 756
QY 265 MetValCysSerCysTyTrpLeuGlnGlyGlnTyGlyValGlnAsnHisTyTrpLeuGlyVal 284
Db 757 CTTCTTACAAATGCTTATCTTGAAGGGAATACGGCTATGAAAGGCACTTACCTTGTGT 816
QY 285 ProCysValIleGlyArgGlyValGluLysIleIleGluLeuLeuThrAlaGln 304
Db 817 CTTACAAATGTAGCGGCAACGCTCTGTAGCAAAATCATTGAACTGAACTGACAGACTAT 876
QY 305 GluArgGlnGluGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAla 324
Db 877 GAAAGCGCAGCTGAATAATCAGTTGATCTGTGCANAAATGTCATGAAGATTATATCC 936

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RESULT 15

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US-10-369-493-41082
; Sequence 41082, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B

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; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 41082
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Bacillus halodurans
US-10-369-493-41082

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Alignment Scores:
Pred. No.: 4,68e-73 Length: 945
Score: 709.00 Matches: 140
Percent Similarity: 65.1% Conservative: 67
Best Local Similarity: 44.0% Mismatches: 97
Query Match: 42.0% Indels: 14
DB: 6 Gaps: 4

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US-09-390-846-2 (1-330) x US-10-369-493-41082 (1-945)

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QY 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
Db 13 CCGAAGAGGTCTCGTTATTGGGGCGGTTTCACAGGTCTACAGACGGCTAATGGTT 72
QY 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMet 45
Db 73 GCTCAAAAGGAATTAGGTGATGCTGTTCTTGTGGAT---ATTCCGCAATGCAAGTCCG 129
QY 46 ProMetGlyLysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThr 65
Db 130 ACTAAAGGAAAGCGTTAGATATGTCGAGTCAACCGCGGTTCAAGGGGTTGATGTGAAC 189
QY 66 ValTyGlySerAsnSerTyGluCysLeuLysGlyAlaAspValValIleThrAla 85
Db 190 ATCAGAGTACGTCTAGCTATGAATATACGAGAGGATTCGATGTTGTTGTCATTACGGT 249
QY 86 GlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuPro 105
Db 250 GGAATTTGCTGTAAGCCTGGT-----ATGAGCGCGATGATCTCGTATCA 294
QY 106 ValAsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyCysProAsnAla 125
Db 295 ACAATTCGGGAATTTATGAAGCTGTTACGAAAGAAAGTGGTGAACATTCACCAACGCC 354
QY 126 PheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSer 145
Db 355 TACATATTGTTTAAACCAACCCACAGATGCGATGACCTATACCCTTTTATAAGAACT 414
QY 146 GlyLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArg 165
Db 415 GGTTCCTCCGAAAAACCGGTCATCGTCAATCGGGGGTCTAGATACGCGACGCTTCCGT 474
QY 166 ArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGly 185
Db 475 ACGTTCGTGCGCAAGAGCTTAACCTATCTGTTGAAGATATTACAGGTTTGTCTTGGG 534
QY 186 ValHisGlyAspHisMetValProLeuSerArgTyAlaThrValAsnGlyIleProLeu 205
Db 535 GGGCAGCGGGATGACATGTCATTCGTTACTCTATGTCAGGTGGGATTCGGCTT 594
QY 206 SerGluPheValLysGlyTrpIleLysGlnGluValAspAspIleValGlnLys 225
Db 595 GAAAGCTC-----CTTCCACAAAGAGCGCATCGATCGGATTTGTGNAACGT 639
QY 226 ThrLysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyTrpAla 245
Db 640 ACGCGCAAAAGCGCGGTAATTCGCGCTTGTCTGGAATGCGAGTCTTATTATGCA 699
QY 246 ProGlyAlaSerAlaIleGlnMetAlaGluSerTyLeuLysAspArgLysArgValMet 265
Db 700 CACGCGCTTCTTTCAGAGATGTCGAAAGCCATCTTCTGAAAGATTAAGAAACGCGCTCT 759

```



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Qy 266 ValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAenHisTyrLeuGlyValPro 285
Db 760 CCAACGATTGCTTACCTTGAAGGTGAGTATGATATGAAGATATCTATGTTGGAGTCCG 819
Qy 286 CysValIleGlyGlyArgGlyValGluGlyIleIleGluLeuGluLeuThrAlaGlnGlu 305
Db 820 ACGATTCTTGGCGGAGACGCCATTGANAAGGTTATTGAGCTTGATCTAACCCGATGAAGAG 879
Qy 306 ArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIle 323
Db 880 AAAGCGACCTTGTCTAAGTCCATTGAATCTGTTCGCAACGTCATGTCGGCACTA 933

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Search completed: March 3, 2006, 00:57:35
Job time : 950 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 3, 2006, 00:57:49 ; Search time 405 Seconds
(without alignments)
1786.381 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVPEKNTKPKIAVGVSGMI.....GSIDVEKEMQKAIKALDASK 330

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7218512 seqs, 1096188070 residues

Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB spool/US09390846/runat 02032006 104245 5144/app query.fasta 1
-DB=Published Applications NA New -QFMT=faetap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03h
-USER=US09390846 @CGN 1.1.220 @runat 02032006 104245 5144 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:*

1: /cg2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cg2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cg2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cg2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cg2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
6: /cg2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
7: /cg2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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12: /cg2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
13: /cg2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----------------------|-------------------|
| 1 | 880.5 | 52.2 | 2862 | 12 US-11-156-953-6 | Sequence 6, Appli |
| 2 | 880.5 | 52.2 | 4716 | 12 US-11-156-953-4 | Sequence 4, Appli |
| 3 | 460 | 27.3 | 1363 | 9 US-11-077-619-51 | Sequence 51, Appl |
| 4 | 418.5 | 24.8 | 969 | 12 US-11-074-176-193 | Sequence 193, App |

| | | | | | |
|----|-------|------|------|-------------------------|-------------------|
| 5 | 408 | 24.2 | 1661 | 8 US-10-947-249-109 | Sequence 109, App |
| 6 | 408 | 24.2 | 1661 | 12 US-11-000-688-1061 | Sequence 1061, Ap |
| 7 | 406 | 24.1 | 1336 | 8 US-10-955-054A-92 | Sequence 92, Appl |
| 8 | 406 | 24.1 | 1336 | 7 US-10-947-249-93 | Sequence 93, Appl |
| 9 | 405 | 24.0 | 1171 | 7 US-10-506-443A-1 | Sequence 1, Appli |
| 10 | 401.5 | 23.8 | 969 | 8 US-10-793-626-1411 | Sequence 1411, Ap |
| 11 | 401.5 | 23.8 | 969 | 8 US-10-793-626-2383 | Sequence 2383, Ap |
| 12 | 401.5 | 23.8 | 3019 | 8 US-10-793-626-4355 | Sequence 4355, Ap |
| 13 | 401.5 | 23.8 | 4093 | 8 US-10-793-626-3793 | Sequence 3793, Ap |
| 14 | 396 | 23.5 | 1317 | 12 US-11-128-061-676 | Sequence 676, App |
| 15 | 396 | 23.5 | 1317 | 12 US-11-128-049-676 | Sequence 676, App |
| 16 | 356 | 21.1 | 1656 | 5 US-09-978-360A-265 | Sequence 265, App |
| 17 | 338.5 | 20.1 | 1053 | 7 US-10-506-443A-2 | Sequence 2, Appli |
| 18 | 338 | 20.0 | 1141 | 6 US-09-925-065A-722171 | Sequence 722171, |
| 19 | 335.5 | 19.9 | 1047 | 7 US-10-506-443A-5 | Sequence 5, Appli |
| 20 | 285.5 | 16.9 | 1280 | 12 US-11-136-527-1594 | Sequence 1594, Ap |
| 21 | 250.5 | 14.8 | 879 | 7 US-10-506-443A-3 | Sequence 3, Appli |
| 22 | 240.5 | 14.2 | 953 | 12 US-11-128-061-348 | Sequence 348, App |
| 23 | 240.5 | 14.2 | 953 | 12 US-11-128-049-348 | Sequence 348, App |
| 24 | 228 | 13.5 | 811 | 7 US-10-506-443A-4 | Sequence 4, Appli |
| 25 | 192.5 | 11.4 | 600 | 12 US-11-128-061-3990 | Sequence 3990, Ap |
| 26 | 192.5 | 11.4 | 600 | 12 US-11-128-049-3990 | Sequence 3990, Ap |
| 27 | 182 | 10.8 | 391 | 8 US-10-821-234-394 | Sequence 394, App |
| 28 | 162.5 | 9.6 | 1225 | 6 US-09-925-065A-26579 | Sequence 26579, A |
| 29 | 161.5 | 9.6 | 1268 | 12 US-11-000-688-1283 | Sequence 1283, Ap |
| 30 | 140 | 8.3 | 1307 | 12 US-11-136-527-38 | Sequence 38, Appl |
| 31 | 129.5 | 7.7 | 600 | 12 US-11-128-061-4318 | Sequence 4318, Ap |
| 32 | 129.5 | 7.7 | 600 | 12 US-11-128-049-4318 | Sequence 4318, Ap |
| 33 | 128.5 | 7.6 | 1637 | 12 US-11-136-527-1710 | Sequence 1710, Ap |
| 34 | 122.5 | 7.3 | 462 | 12 US-11-108-172-164 | Sequence 164, App |
| 35 | 110 | 6.5 | 1400 | 12 US-11-136-527-5806 | Sequence 5806, Ap |
| 36 | 108.5 | 6.4 | 412 | 12 US-11-108-172-652 | Sequence 652, App |
| 37 | 107 | 6.3 | 492 | 5 US-09-995-493-195 | Sequence 195, App |
| 38 | 106 | 6.3 | 389 | 8 US-10-821-234-381 | Sequence 381, App |
| 39 | 94.5 | 5.6 | 861 | 8 US-10-467-657-2767 | Sequence 2767, Ap |
| 40 | 93 | 5.5 | 1336 | 12 US-11-195-459-24 | Sequence 24, Appl |
| 41 | 92.5 | 5.5 | 1362 | 12 US-11-074-176-141 | Sequence 141, App |
| 42 | 92 | 5.5 | 1605 | 8 US-10-646-283-1 | Sequence 1, Appli |
| 43 | 91 | 5.4 | 1065 | 8 US-10-793-626-3097 | Sequence 3097, Ap |
| 44 | 91 | 5.4 | 3320 | 8 US-10-793-626-3649 | Sequence 3649, Ap |
| 45 | 91 | 5.4 | 3690 | 8 US-10-793-626-3439 | Sequence 3439, Ap |

ALIGNMENTS

RESULT 1
US-11-156-953-6
; Sequence 6, Application US/11156953
; Publication No. US20060003051A1
; GENERAL INFORMATION:
; APPLICANT: Cleary, Joseph
; APPLICANT: Coleman, Russell
; APPLICANT: Harding, Nancy
; APPLICANT: Patel, Yamini
; TITLE OF INVENTION: GENETICALLY PURIFIED GELLAN GUM
; FILE REFERENCE: 012047.00029
; CURRENT APPLICATION NUMBER: US/11/156.953
; CURRENT FILING DATE: 2005-06-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2862
; TYPE: DNA
; ORGANISM: Spingomonas elodea
US-11-156-953-6

Alignment Scores:
Pred. No.: 2.86e-94 Length: 2862
Score: 880.50 Matches: 173
Percent Similarity: 70.7% Conservative: 54
Best Local Similarity: 53.9% Mismatches: 89
Query Match: 52.2% Indels: 5
DB: 12 Gaps: 1

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US-09-390-846-2 (1-330) x US-11-156-953-6 (1-2862)
; Sequence 4, Application US/11156953
; Publication No. US2006003051A1
; GENERAL INFORMATION:
; APPLICANT: Cleary, Joseph
; APPLICANT: Coleman, Russell
; APPLICANT: Harding, Nancy
; APPLICANT: Patel, Yamin
; TITLE OF INVENTION: GENETICALLY PURIFIED GELLAN GUM
; FILE REFERENCE: 012047.00029
; CURRENT APPLICATION NUMBER: US/11/156,953
; CURRENT FILING DATE: 2005-06-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4716
; TYPE: DNA
; ORGANISM: Spingomonas elodea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1591)...(3450)
; US-11-156-953-4

Alignment Scores:
Pred. No.: 5.39e-94 Length: 4716
Score: 880.50 Matches: 173
Percent Similarity: 70.7% Conservative: 54
Best Local Similarity: 53.9% Mismatches: 89
Query Match: 52.2% Indels: 5
DB: 12 Gaps: 1

US-09-390-846-2 (1-330) x US-11-156-953-4 (1-4716)
Qy 9 ArgProlylIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 3735 CGCAAGAGATCGCGCTCGATCGGTCGCGATGATCGGTCACCTCGCCACCTCGCT 3794
Qy 29 SerLeuArgGluLeuGlyAspValValPheAspValProAsnMetProMetGly 48
Db 3795 GCATCAAGNACTGGCGGATATGCTCTGTTGCACATTCGCGAGGGCAGCCGCGAGGC 3854
Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly 68
Db 3855 AAGCGCTCGACATCGCACATGTCGCGACCGCTCGAAGGCTTCGATGCGCAACCTCAAGGCG 3914
Qy 69 SerAsnSerTyGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr 88
Db 3915 GCGAACAGCTACGAGGACATTCGCGGCGCGACGCTGTCATCGTCACCGCGGATCCG 3974
Qy 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
Db 3975 CGCAAGCGGCGC-----ATGAGCGCGGACGATCTTCTCAAGCAACACCTG 4019
Qy 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyCysProAsnAlaPheValIle 128
Db 4020 GGCGTGATGAAGCGCTGGCGGAGGATCGCGGCGACGCGCGCGCGCGCGCGTTCGTGATC 4079
Qy 129 AsnIleThrAnProLeuAspValMetValAlaIleGluGlnSerSerGlyLeuPro 148
Db 4080 TGCATACCAACCGCGCTCGACGCGATGTTGGGCGCTGCGCGGCTTCCTGGGCGCTGCG 4139
Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
Db 4140 CACCAAGAGTCGCGGATCGCGGCGTGTCTGACTCGGCGCGCTTCGCGACCTTCCTC 4199
Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
Db 4200 GCCGAGGAATCAACGCTCTCGGTCTCGAGGACGTCACCGCGCTTCGTGCTGGGCGGACACGCG 4259
Qy 189 AspHisMetValProLeuSerArgTyAlaThrValAsnGlyIleProLeuSerGluPhe 208
Db 4260 GACACCATGGTCCCGGTGATCGAGTATTCGACCGCTCGCGCGATCCCCGGTCCCCGACCTG 4319
Qy 209 ValLysLysGlyTyTrpIleLysGlnGluValAspIleValGlnLysThrLysVal 228

US-09-390-846-2 (1-330) x US-11-156-953-6 (1-2862)
Qy 9 ArgProlylIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 1881 CGCAAGAGATCGCGCTCGATCGGTCGCGATGATCGGTGGCACCTCGCGCACCTCGCT 1940
Qy 29 SerLeuArgGluLeuGlyAspValValIlePheAspValProAsnMetProMetGly 48
Db 1941 GCAATCAAGAACTGGGCGATATGCTCTGTCACATTCGCGAGGGCAGCCCGAGGCG 2000
Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly 68
Db 2001 AAGCGCTCGACATCGCACATTCGCGGCGCTCGAGGCTTCGATGCGCAACCTCAAGGCG 2060
Qy 69 SerAsnSerTyGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr 88
Db 2061 CGCAACAGCTACGAGGACATTCGCGGCGCGCGATCTGATCGTCACCGCGGTATCCG 2120
Qy 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
Db 2121 CGCAAGCGGCGC-----ATGAGCGCGGACGATCTTCTCAAGCAACCACTG 2165
Qy 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyCysProAsnAlaPheValIle 128
Db 2166 GCGGTGATGAAGCGCTGGCGAGGCGATCGCGGCGACGCGCGCGCGCTTCGTGATC 2225
Qy 129 AsnIleThrAnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro 148
Db 2226 TGCATCAACCAACCGCTCGACGCGATGTTGGGCGCTGCGGAGTTCCTCGGCGCTGCG 2285
Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
Db 2286 CACCAAGAGTCTCGCGATGTCGCGCGCTGCTCGACTCGCGCGCTTCGCGCACTTCCTC 2345
Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
Db 2346 GCGGAGGAATTCACGCTTCGTCGAGGACGTCACCGCTTCGTCGCGCGCGCGCGCGCG 2405
Qy 189 AspHisMetValProLeuSerArgTyAlaThrValAsnGlyIleProLeuSerGluPhe 208
Db 2406 GACACCATGGTCCCGGTGATCGAGTATTCGACCGCTCGCGGCGATCCCGGTGCGCGACCTG 2465
Qy 209 ValLysLysGlyTyTrpIleLysGlnGluValAspIleValGlnLysThrLysVal 228
Db 2466 ATCAAGATGGGTGCTCCACCGAGCGCGATCGACCGCATCGTCGCGCGCGCGCGCGCTG 2525
Qy 229 AlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyTrpAlaProGlyAla 248
Db 2526 GCGCGCGCGGAGATCGTCGCTGCTCAAGACCGCTCGGCGCTATATGCGCGCGCGCGCG 2585
Qy 249 SerAlaIleGlnMetAlaGluSerTyLeuLysAspArgLysArgValMetValCysSer 268
Db 2586 AGCGCGATCGCGATGGCGGAGCTATCTGAAGGACAAAGAGCGCTGCTTCCTGTGCGC 2645
Qy 269 CysTyTrpLeuGlnGlyGlnTyTrpGlyValGlnAsnHisTyLeuGlyValProCysValIle 288
Db 2646 GCGCACCTCACCGCGCGAGTACGCGCTCGACGATCTGTACGTCGCGGCTGCGCGATC 2705
Qy 289 GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308
Db 2706 GCGAAGGACGCGCTCGAGGCGATCTCGAGATCGAGCTGAACCGCGCGGAGGAGAT 2765
Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAspAla 328
Db 2766 TTCGAGCTCTCGTCTGATCGGTCGAAGAACTGGTTCGCGAGCATGCAAGTTCGATCGACGCC 2825
Qy 329 Ser 329
Db 2826 TCG 2828

RESULT 2
US-11-156-953-4
```

```

Db      4320 ATCAAGATGGGTGGTCCACCAGGAGCGCATCGACGCCATCGTTCGGCGCACCGCTCG 4379
Qy      229 AlaGlyGlyGluValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
Db      4380 GCGCGCGCGGAGATCGTCGCGTCTCAAGACCGGCTCGGCTTATTATGCGCGCGCCACC 4439
Qy      249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
Db      4440 ACGCGGATCGGATGGCGGAGAGCTATCTGAAGGACAAGACGCGCTGCTTCCTGTGCG 4499
Qy      269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
Db      4500 GCGCACCTCACCAGGACGATCGCGTCGACGATCTGTAGCTCGGCTGCGGATCGTCATC 4559
Qy      289 GlyGlyArgGlyValGluLysIleLeuLeuGluLeuThrAlaGlnGluArgGlnGlu 308
Db      4560 GCGAAGGACGGCGTCGAGCGCATCGTCGAGATCGAGCTGAACGCCACCGCGAAGCAGAT 4619
Qy      309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAspAla 328
Db      4620 TTCGAGCTCTCGGTGCGTCAAGGAACTGGTGCAGCATGCAAGTCGATCGATCGACGCC 4679
Qy      329 Ser 329
Db      4680 TCG 4682

```

RESULT 3

```

US-11-077-619-51
; Sequence 51, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Feesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: DE 10242433.0
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Bacillus subtilis
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1363)
; OTHER INFORMATION: 1dh
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1166)
US-11-077-619-51

```

Alignment Scores:

```

Pred. No.: 1,78e-44 Length: 1363
Score: 460.00 Matches: 106
Percent Similarity: 55.2% Conservative: 69
Best Local Similarity: 33.4% Mismatches: 124
Query Match: 27.3% Indels: 18
DB: Gaps: 7

```

US-09-390-846-2 (1-330) x US-11-077-619-51 (1-1363)

Qy 11 LysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCysSerLeu 30

```

Db      222 AAAGTAGCTTTAATCGGAGCGGTTTGTGTGAACAGTATTGCGTAAATTAAC 281
Qy      31 ArgGluLeuGlyAsp---ValValLeuPheAspValValProAsnMetProMetGlyLys 49
Db      282 CAAGGATACACAGATGAGCTTGTGCTCATGTATGATGTAATAAAGAAAAAGCAATGGCGAT 341
Qy      50 AlaMetAspIleSerHisAsnSerSerValValAspThrGlyIle-----Thr 65
Db      342 GTGATGGATTACCCACGGAAGCGTTT-----GGGCTACAACCGGTCAAAACA 392
Qy      66 ValTyrGlySerAsnSerTyrCysLeuLysGlyAlaAspValValIleIleThrAla 85
Db      393 TCTTACGGA-----ACATATGAACACTGCAAGGATGCTGATATTGTCTGCATTTGCGCC 446
Qy      86 GlyIleThrLysIleProGlyLysSerAspLysGluTyrPsrArgMetAspLeuLeuPro 105
Db      447 GGAGCAACACCAAAACCTGGTGAG-----ACACGCTTGAATTAGTAGNA 491
Qy      106 ValAsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAla 125
Db      492 AAGAACTTGAAGATTTTCAAGGCATCGTTAGTGAAGTCATGGCGAGCGGATTTGACGCC 551
Qy      126 PheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSer 145
Db      552 ATTTTCTTAGTCGCGACAAATCCGGTTGATATCTCTGACTTACGCAACATGGAAATTCAGC 611
Qy      146 GlyLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArg 165
Db      612 GGCCTGCCAAAGACCGCGGTGATTGGAAGCGGCACACACTTGATTCGCGAGATTCCT 671
Qy      166 ArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGly 185
Db      672 TTCATGCTGAGCGAATACTTTGGCGCAGCGCTCAAAACGTACACCGCATATTATCGGA 731
Qy      186 ValHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeu 205
Db      732 GAGCACGCGCACACAGACTTCTCTGTTGGAGCCACGCAATGTCCGCGGTGTGCGCGTC 791
Qy      206 SerGluPheValLysGly---TyrIleLysGlnGluGluValAspAspIleValGln 224
Db      792 AGTGAATCTGTTGAAAAACGATCGCTACAAACAGAGAGCTGCGCAAAATTTGTAGAT 851
Qy      225 LysThrLysValAlaGlyGlyGlyValArgLeuLeuGlyGlnGlySerAlaTyrTyr 244
Db      852 GATGTGAAAAACGCGACTTACCATATCATTCAG-----AAAAAGGCGCGACTTATTAT 905
Qy      245 AlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgVal 264
Db      906 GGGGTTCGATGAGTCTTGTCTCGCATTAACAAAAGCCATCTTTCATAATGAAAAACAGCATA 965
Qy      265 MetValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyVal 284
Db      966 TTAATCTGCACACATATTTGGACGGCAATACGCGTCGAGATGCGTGTACATCGTGTG 1025
Qy      285 ProCysValIleGlyGlyArgValGluLysIleLeuLeuGluLeuThrAlaGln 304
Db      1026 CCGGCTGTCGTGAATCGCGGAGGGATCGCAGGTATCACTGAGCTGAACCTTAATGAGAAA 1085
Qy      305 GluArgGlnGluGlnGlySerIleAspGluValLysGluMetGlnLys 321
Db      1086 GAAAAAGAACAGTTCCTTTCACAGCGCGCGCTCTTAAAAACATTTTAAAA 1136

```

RESULT 4

```

US-11-074-176-193
; Sequence 193, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate

```

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore

; FILE REFERENCE: 5051-694

; CURRENT APPLICATION NUMBER: US/11/074,176

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: 60/551,161

; PRIOR FILING DATE: 2004-03-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 193

; LENGTH: 969

; TYPE: DNA

; ORGANISM: Lactobacillus acidophilus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(969)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (0)...(0)

; OTHER INFORMATION: ORF 271; L-lactate dehydrogenase; L-LDH

US-11-074-176-193

Alignment Scores:

Pred. No.: 1,048-39 Length: 969
Score: 418.50 Matches: 101
Percent Similarity: 56.3% Conservative: 83
Best Local Similarity: 30.9% Mismatches: 124
Query Match: 24.8% Indels: 19
DB: 12 Gaps: 10

US-09-390-846-2 (1-330) x US-11-074-176-193 (1-969)

QY 1 MetAlaValPheGluLysAsnThrArgProLysIleAlaMetValGlySerGlyMetIle 20
DB 1 ATGGCAAGAGTTGAAAACCTCGT-----AAAGTTATTATTAGTTGGTGACGGTCTGTA 54
QY 21 GlyGlyThrMetAlaPheLeuCysSerLeuArgGluLeuGly-----AspValVal 37
DB 55 GGTTCCTACCTTTGCAATTT-----TCAATGGTGCAACAGGTATTGCTGAAGAATTAGGT 108
QY 38 LeuPheAspValProAsnMetProMetGlyLysAlaMetAspIleSerHisAsnSer 57
DB 109 ATCATTTGATTGCTTAAGAACACAGTTGAGGTGACGCAATCATCTTAGCA---GATGCT 165
QY 58 SerValValAspThrGlyIleThrValTyrglySerAsnSerTyrgluCysLeuLysGly 77
DB 166 ACTCCATGGACTTTCCAAAGAACATTTACGCGAGCTGACTACGCTGACTGC---AAGGAC 222
QY 78 AlaAspValValIleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGlu 97
DB 223 GCAGACTTAGTAGTTATTACTGCTGCTGCCACAAAAGCCAGGTGAA-----270
QY 98 TrpSerArgMetAspLeuLeuProValAsnIleLysIleMetArgGlu---ValGlyAla 116
DB 271 ---ACTGCTTGACCTGTTTAAACAGACTTGAAGATTTTATCATCATCTGTTGACCA 327
QY 117 AlaIleLysSerTyrglyProAsnAlaPheValIleAsnIleThrAsnProLeuAspVal 136
DB 328 GTTGTGTAATCAGGCTTTGAAGGTATCTTCTTAGTA---GTTGCTAAACCCAGTTGACATC 384
QY 137 MetValAlaAlaLeuGlnGlnSerSerGlyLeuProHisIleArgIleCysGlyMetAla 156
DB 385 TTGACTCAGCACTTTGGAAGATTTCAGGCTTCCCTAAGGATCGCGTTATTGCTTCAGGT 444
QY 157 GlyMetLeuAspSerSerArgPheArgMetIleAlaAspLysLeuGluValSerPro 176
DB 445 ACTTCACTTGATGCTGCTCTTCAAAAGGTTATCGTTAAGTGAACACAGCTTGACCA 504
QY 177 ArgAspValGlnGlyMetValIleGlyValHisGlyAspHisMetValProLeuSerArg 196
DB 505 CGTTCAGTTAATGCATACATGCTTGTGTAACACGGGTGACTGAATTCACGATGAGAC 564
QY 197 TyrAlaThrValAsnGlyIleProLeuSerGluPheValLysGlyTrpIleLysGln 216

DB 565 TACAACAATGTTGCTGGCGTAAGAGTTAGCGACTGGGTTAAGGCTCACGGTATGGATGAA 624
QY 217 GluGluValAspAspIleValGlnLysThrLysValAlaGlyGlyGluIleValArgLeu 236
DB 625 TCTAAGCTTGAAGAAATCCACAAGGAAGTTGCTGACATGGCTTACGACATTTATCAAC--- 681
QY 237 LeuGlyGlnGlySerAlaTyrtyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSer 256
DB 682 ---AAGAAGGGTGCTACTTTCTAGGTTATCGGTATCGGTATCGGTATCGGTATCGGTATCGGT 738
QY 257 TyrLeuLysAspArgLysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyrgly 276
DB 739 ATCTTGAACGATGAACACCGGTACTTCCACTCTCAGTTGCAATGGATGGTCAATACGGT 798
QY 277 ValGlnAsnHisTyrLeuGlyValProCysValIleGlyGlyArgGlyValGluLysIle 296
DB 799 TTACACGACCTTCACATTTGGTACTCTCTGCGATTTGTTGGCCGTAACGGTCTTTGAACAAAT 858
QY 297 IleGluLeuGluLeuThrAlaGlnGluArgGlnGluLeuGlnGlySerIleAspGluVal 316
DB 859 ATTGAATGCTTTTAAACCGCTGATGAACAAGCTAAGATGGAAGCTTCTGCTAAGCAATTA 918
QY 317 LysGlu---MetGlnLysAla 322
DB 919 AAGGAGTTATGGACAAGGCC 939

RESULT 5

US-10-947-249-109

; Sequence 109, Application US/10947249

; Publication No. US20050287541A1

; GENERAL INFORMATION:

; APPLICANT: Akira NAKAGAWARA

; APPLICANT: Mikio OHIRA

; APPLICANT: Shin ISHII

; APPLICANT: Takeshi GOTO

; APPLICANT: Hiroyuki KUBO

; APPLICANT: Takahiro HIRATA

; APPLICANT: Yasuko YOSHIDA

; APPLICANT: Saichi YAMADA

; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma

; FILE REFERENCE: 117007

; CURRENT APPLICATION NUMBER: US/10/947,249

; PRIORITY FILING DATE: 2004-09-23

; PRIOR APPLICATION NUMBER: US 60/505,614

; PRIOR APPLICATION NUMBER: 2003-09-25

; NUMBER OF SEQ ID NOS: 200

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 109

; LENGTH: 1661

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-947-249-109

Alignment Scores:

Pred. No.: 3,71e-38 Length: 1661
Score: 408.00 Matches: 102
Percent Similarity: 53.6% Conservative: 71
Best Local Similarity: 31.6% Mismatches: 138
Query Match: 24.2% Indels: 12
DB: 8 Gaps: 7

US-09-390-846-2 (1-330) x US-10-947-249-109 (1-1661)

QY 5 GluLysAsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMet 24
DB 143 GAACAGACCCCAAGATTAAGATTTGTTGGGTTGGTGTGGTGGTGGTGGTGGTGGTGGT 202
QY 25 AlaPheLeuCysSerLeuArgGluLeuGlyAsp---ValValLeuPheAspValValPro 43
DB 203 GCCATCATGATCTTAAATGAAGAGCTTGGCAGATGAATCTTGTCTTGTGTGATGTCGAA 262

| | | | |
|----|------|---|------|
| Qy | 44 | AsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValValAspThrGly | 63 |
| Db | 263 | GACAAATTGAAGGGAGAGATGATGGATCTCCAACATGCGACCTTTTCCCTTAGAACACCA | 322 |
| Qy | 64 | IleThrValTyrGlySerAsnSerTyrClucCysLeuLysGlyAlaAspValValIleIle | 83 |
| Db | 323 | AAGATTGTCTCTGGCAAGAC--TATAATGTAATCTGCAAACTCCAAGCTGGTCATTATC | 379 |
| Qy | 84 | ThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeu | 103 |
| Db | 380 | ACGCTGGGCACGCTCAGCAAGAGGAGAA-----ACCGCTCTTAATTG | 424 |
| Qy | 104 | LeuProValAsnIleLysIleMetArgGluValGlyAlaIleLysSerTyrCysPro | 123 |
| Db | 425 | GTCCAGCGTAACTGGAACATATTAAATTCATCTTCCTAATGTTGTAAATAACAGCCG | 484 |
| Qy | 124 | AsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGlu | 143 |
| Db | 485 | AACATGCAAGTTGCTATTGTTTCCAAATCCAGTGGATATCTTGACCTACGTGGCTTGAAG | 544 |
| Qy | 144 | SerSerGlyLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArg | 163 |
| Db | 545 | ATAAGTGGTTTTCCCAAAACCGTGTTATTGGAAGTGGTTCGAATCTGGAAATTCAGCCCGA | 604 |
| Qy | 164 | PheArgArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetVal | 183 |
| Db | 605 | TTTCGTTACCTGATGGGGAAAGCGTGGAGTTCAACCATTAAGCTGTCATGGTGGGTC | 664 |
| Qy | 184 | IleGlyValHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIle | 203 |
| Db | 665 | CTTGGGAAACATGGAGATTCCAGTGTGCCTGTATGGAGTGGATGAATGTTGCTGGTGT | 724 |
| Qy | 204 | ProLeuSerGluPhe---ValLysLysGlyTrpIleLysGlnGluGluValAspAspIle | 222 |
| Db | 725 | TCTCTGAAGACTCTGCACCCAGATTTAGGCACTGATAAAGATAAGAACAGTGGAAAGAG | 784 |
| Qy | 223 | ValGlnLysThrLysValAlaGlyGly---GluIleValArgLeuLeuGlyGlnGlySer | 241 |
| Db | 785 | GTTCCACAGCAGGTGGTTGAGAGTCTTATGAGGTGATCAAACTCAAGGCTACACATCC | 844 |
| Qy | 242 | AlaTyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArg | 261 |
| Db | 845 | -----TGGGCTATTGGACTCTCTGTAGCAGATTGGCAGAGAGTATAATGAAGAATCTT | 898 |
| Qy | 262 | LysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHis--- | 280 |
| Db | 899 | AGCGGGTGACCCAGTTTCCACCATTGAAGGCTCTTTACGGAATAAAGAGTATGATGTC | 958 |
| Qy | 281 | TyrLeuGlyValProCysValIleGlyGlyArgGlyValGluLysIleIleGluLeuGlu | 300 |
| Db | 959 | TTCTTAGTGTCTCTGCATTTTGGGACAGAATGGAATCTCAGACCTTGTGAAGGTGACT | 1018 |
| Qy | 301 | LeuThrAlaGlnGluArgGlnGlnGlnGlnGlnSerIleAspGluValLysGluMetGln | 320 |
| Db | 1019 | CTGACTCTCAGGAAGAGGCCGCTTTCGAAGAGAGTGCAGATACACTTTGGGGGATCCAA | 1078 |
| Qy | 321 | LysAlaIle 323 | |
| Db | 1079 | AAGGAGCTG 1087 | |

RESULT 6

```

; RESULT 6
US-11-000-688-1061
; Sequence 1061, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987

```

```

Qy 242 AlaTyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArg 261
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Db 845 -----TGGGCTATTGGACTCTCTGTAGCAGATTGGCAGAGATTAATAAGAAATCTT 898
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Qy 262 LysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHis--- 280
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Db 899 AGCGGGTGCACCCAGTTTCCACCATGATTAAAGGCTCTTTACGGNATAAAGATGATGTC 958
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Qy 281 TyrLeuGlyValProCysValIleGlyArgGlyValGluLysIleIleGluLeuGlu 300
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Db 959 TTCCTTAGTGTCTTGTGATTTGGGACAGAAATCGAATCTCAGACCTTGTGAAGTGACT 1018
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Qy 301 LeuThrAlaGlnGluArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGln 320
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Db 1019 CTGACTTCTGAGGAAGAGCCCGTTTGAAGAAGAGTGCAGATACACTTTGGGGGATCCAA 1078
   ::::: ||| ||| ::::: ||| ||| ::::: ||| ||| ::::: ||| |||
Qy 321 LysAlaIle 323
   ::::: ||| |||
Db 1079 AAGGAGCTG 1087

RESULT 7
US-10-955-054A-92
; Sequence 92, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 92
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-92

Alignment Scores:
Pred. No.: 4,87e-38 Length: 1336
Score: 406.00 Matches: 99
Percent Similarity: 51.5% Conservative: 75
Best Local Similarity: 29.3% Mismatches: 130
Query Match: 24.1% Indels: 34
DB: 8 Gaps: 10

US-09-390-846-2 (1-330) x US-10-955-054A-92 (1-1336)

Qy 5 GluLysAsnThrArgPro-----LysIleAlaMetValGlySerGlyMetIleGlyGly 22
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 145 GAAGAGCAACAGATTCCAAACAAATAAGATCACTAGTGGGTGTGGCAAGTTGCT--- 201
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 23 ThrMetAlaPheLeuCysSerLeuArgGluLeuGly-----AspValVal 37
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 202 -----ATGCGTGTCTATCAGCATTTCTGGGAAAGCTCTCTGCGTCACTGCTGCT 252
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 38 LeuPheAspValProAsnMetProMetGlyLysAlaMetAspIleSerHisAsnSer 57
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 253 CTTGTGGATGTTTGAAGATAAGCTTAAAGGAGAAATATGATGATCTGCAGCATGGGAGC 312
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 58 SerValValAspThrGlyIleThrValTyrGlySerAsnSerTyrGluCysLeuLysGly 77
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 313 TTATTTCTCAGACACT---AAAATTGGCGCAGATAAAGATTATCTGTGACCGCCAAT 369
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 78 AlaAspValValIleIleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGlu 97
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 370 TCTAAGATTGTAGTGAATCTGAGGAGTCCGTCAGCAAGAAGGGGAG----- 417
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 98 TrpSerArgMetAspLeuLeuProValAsnIleLysIleMetArgGluValGlyAlaAla 117

```

```

Db 418 ---AGTCGGCTCAATCTGGTGCAGAGAAATGTTAATCTCTTCAAATTCATTATTCCTCAG 474
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 118 IleLysSerTyrCysProAsnAlaPheValIleAsnIleThrAsnProLeuAspValMet 137
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 475 ATCGTCAAGTACAGTCTGATTCATCATTAATTTGGTTTCCCAACCCAGTGGACATCTT 534
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 138 ValAlaIleGlnGluSerSerGlyLeuProHisIleGlyCysGlyMetAlaGly 157
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 535 ACGTATGTTACCTGGAAACAAAGTGGATTACCCAAACACCCGCGTGAATGGAGTGGATGT 594
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 158 MetLeuAspSerSerArgPheArgMetIleAlaAspLysLeuGluValSerProArg 177
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 595 AATCTGATTTCTGATGTTTCTGCTACCTTATGCTGAAACCTTGGCATTCATCCACG 654
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 178 AspValGlnGlyMetValIleGlyValHisGlyAspHisMetValProLeuSerArgTyr 197
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 655 AGCTGCCATGGATGGATTTTGGGGGAAACATGGCGACTCAAGTGTGGTGTGGAGTGGT 714
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 198 AlaThrValAsnGlyIleProLeuSerGluPhe-----Val 209
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 715 GTGAATGTGGCAGGTGTTCTCTCCAGGAATTGAATCCAGAAATGGGAACTGACAATGAT 774
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 210 LysLysGlyTrpIleLysGlnGluValAspIleValGlnLysThrLysValAla 229
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 775 AGTGAATAATGG-----AAGGAAGTGCATAAGATGGTGGTTGAAAGTGCCTAT--- 822
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 230 GlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAlaSer 249
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 823 -----GAAGTCATCAAGCTA-----AAAGGATATACCAACTGGGCTATTGGATTAAGT 870
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 250 AlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSerCys 269
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 871 GTGCTGATCTTATTGAATCCATGTTGAAATAATCTATCCAGGATTCATCCCGTGTCAACA 930
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 270 TyrLeuGlnGlyGlnTyrGlyValGlnAsnHis---TyrLeuGlyValProCysValIle 288
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 931 ATGTTAAAGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 990
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 289 GlyGlyArgGlyValGluLysIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 991 AATGCCGGGATTAAACCCAGCGTTATCAACCAAGAGCTAAAGAGTATGATGATGATGAT 1050
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeu 326
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||
Db 1051 CTCAGAAAGAGTGCAGATACCTCTGGGACATCCAGAGGACCTTAAAGACCTG 1104
   |||::: ||| ||| |||::: ||| ||| |||::: ||| ||| |||::: ||| |||

RESULT 8
US-10-947-249-93
; Sequence 93, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: AKIRA NAKAGAWARA
; APPLICANT: MIKI OHIRA
; APPLICANT: SHIN ISHII
; APPLICANT: TAKESHI GOTO
; APPLICANT: HIROYUKI KUBO
; APPLICANT: TAKAHIRO HIRATA
; APPLICANT: YASUKO YOSHIDA
; APPLICANT: SAICHI YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 93
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens

```


US-10-947-249-93

Alignment Scores:

Pred. No.: 4,87e-38 Length: 1336
Score: 406.00 Matches: 99
Percent Similarity: 51.5% Conservative: 75
Best Local Similarity: 29.3% Mismatches: 130
Query Match: 24.1% Indels: 34
Gaps: 10

US-09-390-846-2 (1-330) x US-10-947-249-93 (1-1336)

QY 5 GluLysAsnThrArgPro-----LysIleAlaMetValGlySerGlyMetIleGlyGly 22
DB 145 GAAGAGGCAACAGTTCACAAACAAATAGATCATCTAGTGGGTGGGAGTTCGT--- 201
QY 23 ThrMetAlaPheLeuCySerLeuArgGluLeuGly-----AspValVal 37
DB 202 -----ATGGCGTGCTATCAGCATCTCGGAAGTCTCTGGCTGATGAATTCGT 252
QY 38 LeuPheAspValProAsnMetProMetGlyLysAlaMetAspIleSerHisAsnSer 57
DB 253 CTGTGGATGTTTGAAGATAAGCTTAAAGGAGAAATGATGATCGCAGCATGGAGC 312
QY 58 SerValValAspThrGlyIleThrValTyrGlySerAsnSerTyrGluCysLeuLysGly 77
DB 313 TTATTTCTTCAGACACCT---AAAAATTGTGCAGATAAAGATTATTCTGTGACCGCCAAT 369
QY 78 AlaAspValValIleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGlu 97
DB 370 TCTAGATGTAGTGTACTCAGAGTCCCTCAGAGAGAGAGGAG----- 417
QY 98 TrpSerArgMetAspLeuLeuProValAsnIleLysIleMetArgGluValGlyAlaAla 117
DB 418 ---AGTCGGCTCAATCTGGTCAGAGAAATGTTAATGCTTCAATTCATTATTCCTCAG 474
QY 118 IleLysSerTyrCyProAsnAlaPheValIleAsnIleThrAsnProLeuAspValMet 137
DB 475 ATCTGCAAGTACAGCTCTGATTCATCATTAATGTGGTTTCCACCAGTGGACATTC 534
QY 138 ValAlaAlaLeuGlnGluSerGlyLeuProHisArgIleCysGlyMetAlaGly 157
DB 535 ACGTATGTACTGGAAATAGTGGATTACCACACCGCGTGAATGGAGTGGAGTGT 594
QY 158 MetLeuAspSerArgPheArgArgMetIleAlaAspLysLeuGluValSerProArg 177
DB 595 AATCTGGATTCGTAGATTCCTACCTATGCTGCTGAAACACTGGCATTCATCCAGC 654
QY 178 AspValGlnGlyMetValIleGlyValHisGlyAspHisMetValProLeuSerArgTyr 197
DB 655 AGCTGCCATGGATGGATTTTGGGGGAACATGGCGACTCAAGTGTGGCTGTGGAGTGT 714
QY 198 AlaThrValAsnGlyIleProLeuSerGluPhe-----Val 209
DB 715 GTGAATGGCAGGTGTCTCTCCAGGAATGAAATCCAGAAATCGGAACCTGACAAATGAT 774
QY 210 LysLysGlyTyrIleLysGlnGluValAspAspIleValGlnLysThrLysValAla 229
DB 775 AGTGAATGG-----NAGNAGTGCAATAGATGGGTGGTGAAGTCCTAT--- 822
QY 230 GlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAlaSer 249
DB 823 -----GAAGTCATCAAGCTA-----AAAGGATATACCACTGGGCTATTGGATTAAGT 870
QY 250 AlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSerCys 269
DB 871 GTGGCTGATCTTATTGAATCCATGTGAAATAATCTATCCAGGATTCATCCCGGTGCAACA 930
QY 270 TyrLeuGlnGlyGlnTyrGlyValGlnAsnHis---TyrLeuGlyValProCysValIle 288
DB 931 ATGGTAAGGGGATGTATGGCATTCAGATGAGTCTTCCTGAGCCTTCATGATATCTC 990
QY 289 GlyGlyArgGlyValGlnLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308

DB 991

AATGCCGGGGAATTAACCAAGCGTTATCAACCAAGCTAAAGGATGATGAGTTCTCTCAG 1050

QY 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaAlaLeu 326
DB 1051 CTCAAGAAAGTGCAGATACCTGTGGGACATCCAGAGGACCTAAAGACCTG 1104

RESULT 9

US-10-506-443A-1

; Sequence 1, Application US/10506443A

; Publication No. US20060013817A1

; GENERAL INFORMATION:

; APPLICANT: Sahin Dr., Ugur

; APPLICANT: Tureci Dr., Ozlem

; APPLICANT: Koglowski Dr., Michael

; TITLE OF INVENTION: Genetic Products Differentially Expressed in Tumors and Use There

; FILE REFERENCE: 342-3PCT

; CURRENT APPLICATION NUMBER: US/10/506,443A

; CURRENT FILING DATE: 2004-09-01

; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1171

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-506-443A-1

Alignment Scores:

Pred. No.: 5,43e-38 Length: 1171
Score: 405.00 Matches: 101
Percent Similarity: 52.9% Conservative: 72
Best Local Similarity: 30.9% Mismatches: 130
Query Match: 24.0% Indels: 24
Gaps: 7

US-09-390-846-2 (1-330) x US-10-506-443A-1 (1-1171)

QY 5 GluLysAsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMet 24
DB 104 GATGAAACTCCAGTGTAAATTAATCTTGGAACTGGTGGCTAGGCATGGCTTGT 163
QY 25 AlaPheLeuCySerLeuArgGluLeuGlyAsp---ValValLeuPheAspValPro 43
DB 164 GCTATTAGTATCTTACTGAAGATTGGCTGTGAACCTTGGCTTGTGTGATGTTGCATTG 223
QY 44 AsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerValValAspThrGly 63
DB 224 GACAACTGAAGGAGAAATGATGATCTTCAGCATGGCAGTCTTTCTTTAGTACTTCA 283
QY 64 IleThrValTyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleIle 83
DB 284 AAGATTACTTCTGGAAAGAT---TACAGTGTATCTGCAAACTCCAGATAGTATTGCTC 340
QY 84 ThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeu 103
DB 341 ACAGCAGGTGCAAGCAGCAGCAGGAGAGAA-----ACTCGCTTCCCTGCT 385
QY 104 LeuProValAsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysPro 123
DB 386 GTCCAACTGAATGGGTATTAATCAATCAATCTCTGCAATAGTCCATTATAGTCTCT 445
QY 124 AsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlu 143
DB 446 GATTGTAATAATCTTGTGTTTCAATCCAGTGGATATTTGACATATATAGTCTGGAG 505
QY 144 SerSerGlyLeuProHisArgIleCysGlyMetAlaGlyMetLeuAspSerArg 163
DB 506 ATAAGTGGCTTACCTGTAACCTCGTGAATTTGGAAGTGGTGTGTAATCTAGACTCTGCCCT 565
QY 164 PheArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetVal 183
DB 566 TTCCGTTACCTAATTTGGAGAAAGTTGGTGTGCCACCCCAAGCTGCCATGGTGGATT 625

184 IleGlyValHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAlaGlyIle 203
 626 ATTGAACATGGTGAATCTAGTGTGCTTATGGAGTGGGTGAATGCTGGT 685
 204 ProLeu-----SerGluPheValLysGlyTyrIleLys 215
 686 GCTCTGAAGACTCTGGACCTAAATTTAGGAACGGATTACAGTAAGAACACTGG----- 739
 216 GlnGluValAlaAspIleValGlnLysThrLysValAlaGlyGlyIleValArg 235
 740 -----AAAAATATCAATAAACAAGTTATTCAAAAGTCCCTATGAATATATCAAG 787
 236 LeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGlu 255
 788 CTGAAGGGGTATACCTCT-----TGGGCTATTGGACTCTCTGATGATCTGGTAGGA 841
 256 SerTyrLeuLysAspArgLysValMetValCysSerCysTyrLeuGlnGlyGlnTyr 275
 842 TCCATTTTCAAAAATCTTAGGAGAGTGACCCAGTTTCCACCATGGTTAAGGGATTATAT 901
 276 GlyValGlnAsnHis---TyrLeuGlyValProCysValIleGlyCysArgGlyValGlu 294
 902 CGAATAAAGAAGAACTCTTTCTCAGTATCCCTTGTGCTCTGGGGCGGAATGGTGTCTCA 961
 295 LysIleIleGluLeuGluLeuThrAlaGlnGluAUGlnGluLeuGlnGlySerIleAsp 314
 962 GATGTTGTGAAAATTAACCTTGAATCTGAGGAGGAGGCCCTTTTCAAGNAGAGTGCAGAA 1021
 315 GluValLysGluMetGlnLys 321
 1022 ACATTTTGGAAATATTCAAAAG 1042

RESULT 10

US-10-793-626-1411
 ; Sequence 1411, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 1411
 ; LENGTH: 969
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-1411

Alignment Scores:
 Pred. No.: 1,12e-37 Length: 969
 Score: 401.50 Matches: 93
 Percent Similarity: 53.0% Conservative: 75
 Best Local Similarity: 29.3% Mismatches: 140
 Query Match: 23.8% Indels: 9
 DB: 8 Gaps: 4

US-09-390-846-2 (1-330) x US-10-793-626-1411 (1-969)

11 LysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCysSerLeu 30
 37 AAAGTTGTTTAGTAGGACCGTCCGATAGTTCAAGTATGATGCTATGCTGACT 96
 31 ArgGluLeuGlyAsp---ValValLeuPheAspValProAsnMetProMetGlyLys 49
 97 CAAGGAATTCAGATGAATTTGTAATTTATTTGATATTTGTAAGAAAGATAAAGTGAAGACAGAC 156

50 AlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrValTyrGlySer 69
 157 GTTAAAGATTAAACCATGGTGCACTTTACAGTTCTTCACCAGTGACGTGA---AAAGCT 213
 70 AsnSerTyrGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThrLys 89
 214 GGAGAATATGAAGATTGTAAGATGCAAGATTAGTTAGTTATTATACAGCAGGTGCACCTCAA 273
 90 IleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsnIleLys 109
 274 AAACCGGGTGAA-----ACTCGTTTACAACTTGTGTGAGAAAATACTATAA 318
 110 IleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValIleAsn 129
 319 ATCATGAAAAGTATCGTAACCTAGTGTGATGATGCTGCTTGTGTTCTTCTCTAATT 378
 130 IleThrAsnProLeuAspValMetValAlaAlaGlnGlnGlnGlnGlnGlnGlnGln 149
 379 GCTGCAAAACCCAGTATATCTTAACACGTTATGTTAAAGAAAGTTACAGGTTTACAGCT 438
 150 HisArgIleCysGlyMetAlaGlyMetLeuAspSerArgPheArgMetIleAla 169
 439 GAACGTGTTATGTTGTTCTGTTACAGTGTGCTGATGATGATGATGATGATGATGATGAT 498
 170 AspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGlyAsp 189
 499 AAAGAAATAGTGTGTTACATCAAGTAGTGTTCACGCTAGCATTTATAGTGAACATGTCAC 558
 190 HisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPheVal 209
 559 TCTGAACCTTCAGATTGTTGCTCTCAAGCAACCGTTGGAGGTATTTTCAGTGTATGATACATTG 618
 210 LysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLysValAla 229
 619 AAAGAAACAACTGGTAGCGATGCTAAAGCGAATGAAATTTATATTAATACAGAGATGCT 678
 230 GlyGlyGluIleValArgLeuGlnGlySerAlaTyrTyrAlaProGlyAlaSer 249
 679 GCTTACGATATCATTCAA-----GCTAAAGGATCTAGCTATTTATGTTAGTCTAGCA 732
 250 AlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSerCys 269
 733 CTATTACGTATTTCTAAAGCTTTACTAAATAATGAAATAGTATTTTTCACAGTTTCTAGT 792
 270 TyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIleGly 289
 793 CAACCTTAATGTCATATGATGATTTAACGATGTTTATCTTGGCTTACCACACTTATCAAT 852
 290 GlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGluLeu 309
 853 CAAGATGGTGCAGTTAAATTTATGAAACACCATTAATGATGATGATGATGATGATGATGAT 912
 310 GlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaAlaLeu 326
 913 GAAAAATCAGTGAAAACTTTAGAGACACTTTATGATCTTATATAAAACATTTA 963

RESULT 11

US-10-793-626-2383
 ; Sequence 2383, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 2383
 ; LENGTH: 969
 ; TYPE: DNA

Db 1329 AAAGAAATTAGTGTACATCAAGTAGTCTTCACGCTAGCATATTATAGGTGAACATGGTGAC 1270
Qy 190 HisMetValProLeuSerArgTyrAlaThrValaenGlyIleProLeuSerGluPheVal 209
Db 1269 TCTGAACCTTGCACTTTGGTCTCAAGCAACCGTTGGAGGTATTTTCAGTGTATGATACATTTG 1210
Qy 210 LysLysGlyTyrIleLysGlnGluValAsePheIleValGlnLysValAla 229
Db 1209 AAAGAAGAACTGGTAGCGATCTAAACCGAATGAATTTATATTATTAACAGAGATGCT 1150
Qy 230 GlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAlaSer 249
Db 1149 GCTTACGATATCAATCAA-----GCTAAAGGATCTAGTATTATGGTATAGCTCTAGCA 1096
Qy 250 AlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSerCys 269
Db 1095 CTATTACGTATTTCTAAAGCTTTTAAATTAATGAATAATAGTATTTTTCACAGTTTCTAGT 1036
Qy 270 TyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIleGly 289
Db 1035 CAACCTTAATGGTCAATATGGATTTAAACGATGTTTATCTTGGCTTACCAACACTTATCAAT 976
Qy 290 GlyArgGlyValGluLysIleIleGluLeuGluThrAlaGlnGluArgGlnGluLeu 309
Db 975 CAAATGGTGCAGTTAAATTTATGAACACCATTAATGAATGATAAGCACTACATTTACTA 916
Qy 310 GlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeu 326
Db 915 GAAAAATCAGTGAACCTTTAGACACACTTATGATTTCTATAAAACATTTA 865

RESULT 13

US-10-793-626-3793
; Sequence 3793, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3793
; LENGTH: 4093
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3793

Alignment Scores:
Pred. No.: 6,98e-37 Length: 4093
Score: 401.50 Matches: 93
Percent Similarity: 53.0% Conservative: 75
Best Local Similarity: 29.3% Mismatches: 140
Query Match: 23.8% Indels: 9
DB: 8 Gaps: 4

US-09-390-846-2 (1-330) x US-10-793-626-3793 (1-4093)

Qy 11 LysIleAlaMetValGlySerGlyMetIleGlyIleThrMetAlaPheLeuCysSerLeu 30
Db 1105 AAAGTGTATTAGTAGGACCGTCCGTAGGTCAAGTATGATTTGCTATGGTGACT 1164
Qy 31 ArgGluLeuGlyAsp---ValValLeuPheAspValProAsnMetProMetGlyLys 49
Db 1165 CAAGGAATTGCAGATGAATTTGTAATTATTTGATATTTGCAAAAGATAAAGTGAAGCAGAC 1224
Qy 50 AlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGlySer 69

Db 1225 GTTAAAGATTAAACCATGGTGCACITTTACAGITTTCTTCACCAGTGAAGCTGTA---AAAGCT 1281
Qy 70 AsnSerTyrGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThrLys 89
Db 1282 GGAGAATATGAAGATTGTAAGATGTCAGATTTAGTTTATTTACAGCAGGTGACCTCAA 1341
Qy 90 IleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsnIleLys 109
Db 1342 AAACCGGGTGA-----ACTCGTTTACAACCTGTTGAGAAAAATACTATA 1386
Qy 110 IleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheValIleAsn 129
Db 1387 ATCATGAAAAAGTATCGTACGTAGTGTCTATGATAGTGGCTTTGATGGTTTCTTCTCAATT 1446
Qy 130 IleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeuProHis 149
Db 1447 GCTCAAAACCCAGTTGATATCTTAAACAGTTATGTTAAAGAAAGTTACAGGTTTACCAGCT 1506
Qy 150 HisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIleAla 169
Db 1507 GAACGTGTTATGTTCTGGTACAGTCTTGTATAGTGCAGATTCAGATATTTAATAAGT 1566
Qy 170 AspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGlyAsp 189
Db 1567 AAGAATTAGTGTTCATCAAGTAGTGTTCACGCTAGCATTTATAGTGAACATGGTGAC 1626
Qy 190 HisMetValProLeuSerArgTyrAlaThrValaenGlyIleProLeuSerGluPheVal 209
Db 1627 TCTGAACCTTGCACTTTGGTCTCAAGCAACCGTTGGAGGTATTTTCAGTGTATGATACATTTG 1686
Qy 210 LysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLysValAla 229
Db 1687 AAAGAAGAACTGGTAGCGATCTTAAGCGAATGAATTTATATTATTAACAGAGATGCT 1746
Qy 230 GlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAlaSer 249
Db 1747 GCTTACGATATCAATCAA-----GCTAAAGGATCTAGTATTATGGTATAGCTCTAGCA 1800
Qy 250 AlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSerCys 269
Db 1801 CTATTACGTATTTCTAAAGCTTTTAAATTAATGAATAATAGTATTTTTCAGAGTTTCTAGT 1860
Qy 270 TyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIleGly 289
Db 1861 CAACCTTAATGGTCAATATGGATTTAAGATGTTTATCTTGGCTTACCAACACTTATCAAT 1920
Qy 290 GlyArgGlyValGluLysIleIleGluLeuGluThrAlaGlnGluArgGlnGluLeu 309
Db 1921 CAAATGGTGCAGTTAAATTTATGAACACCATTAATGAATGAACAACTACAAATTACTA 1980
Qy 310 GlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeu 326
Db 1981 GAAAAATCAGTGAACCTTTAGACACACTTATGATTTCTATAAAACATTTA 2031

RESULT 14

US-11-128-061-676
; Sequence 676, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 23:58:53 ; Search time 207 Seconds
(without alignments)
2833.794 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688
Sequence: 1 MAVPEKTRPIAMVSGMI.....GSIDEVKEMQKAIADLASK 330

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abss/ABSSWEB spool/US09390846/runat 02032006 104236 4927/app query.fasta_1
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCALALIGN=pco -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss03p -USER=US09390846 @CGN 1 1 290 @runat 02032006 104236 4927
-NCPU=6 -ICPU=3 -NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
6: /cgn2_6/ptodata/1/ina/ECTUS COMB.seq:*
7: /cgn2_6/ptodata/1/ina/pp COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 1688 | 100.0 | 1679 | 3 | US-08-676-882-1 |
| 2 | 1034.5 | 61.3 | 1785 | 3 | US-09-216-393B-311 |
| 3 | 1034.5 | 61.3 | 1785 | 3 | US-09-216-393B-313 |
| 4 | 831.5 | 49.3 | 951 | 6 | PCT-US94-03796-1 |
| 5 | 706 | 41.8 | 1912 | 2 | US-08-270-013B-1 |
| 6 | 706 | 41.8 | 1912 | 2 | US-08-838-418-1 |
| 7 | 694 | 41.1 | 1870 | 3 | US-09-902-540-6244 |
| 8 | 694 | 41.1 | 1634 | 3 | US-09-902-540-341 |
| 9 | 641 | 38.0 | 978 | 3 | US-09-134-001C-2696 |

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|----|-------|------|--------|---|---------------------|-------------------|
| 10 | 632 | 37.4 | 5024 | 2 | US-08-920-812-7 | Sequence 7, Appli |
| 11 | 632 | 37.4 | 5024 | 2 | US-08-920-827-7 | Sequence 7, Appli |
| 12 | 632 | 37.4 | 5024 | 2 | US-08-921-177-7 | Sequence 7, Appli |
| 13 | 632 | 37.4 | 5024 | 2 | US-08-362-577C-7 | Sequence 7, Appli |
| 14 | 632 | 37.4 | 5024 | 2 | US-08-920-828-7 | Sequence 2832, Ap |
| 15 | 464 | 27.5 | 975 | 3 | US-09-107-532A-2832 | Sequence 1, Appli |
| 16 | 434.5 | 25.7 | 580073 | 3 | US-08-545-528D-1 | Sequence 1012, Ap |
| 17 | 426 | 25.2 | 957 | 3 | US-09-134-000C-1012 | Sequence 36, Appl |
| 18 | 408 | 24.2 | 1661 | 3 | US-09-166-350-31 | Sequence 1340, Ap |
| 19 | 408 | 24.2 | 1661 | 3 | US-09-220-132-36 | Sequence 22, Appl |
| 20 | 408 | 24.2 | 1661 | 3 | US-09-023-655-1340 | Sequence 2131, Ap |
| 21 | 406 | 24.1 | 1260 | 3 | US-09-166-350-22 | Sequence 5381, Ap |
| 22 | 406 | 24.1 | 1383 | 3 | US-09-949-016-2131 | Sequence 5382, Ap |
| 23 | 405 | 24.0 | 1173 | 3 | US-09-949-016-5381 | Sequence 1411, Ap |
| 24 | 405 | 24.0 | 1173 | 3 | US-09-949-016-5382 | Sequence 1411, Ap |
| 25 | 401.5 | 23.8 | 969 | 3 | US-09-710-279-1411 | Sequence 1491, Ap |
| 26 | 401.5 | 23.8 | 969 | 3 | US-09-710-279-2383 | Sequence 4355, Ap |
| 27 | 401.5 | 23.8 | 993 | 3 | US-09-134-001C-1491 | Sequence 57, Appl |
| 28 | 401.5 | 23.8 | 3019 | 3 | US-09-710-279-4355 | Sequence 620, App |
| 29 | 401.5 | 23.8 | 4093 | 3 | US-09-710-279-3793 | Sequence 1, Appli |
| 30 | 396.5 | 23.5 | 14333 | 3 | US-08-956-171E-57 | Sequence 2149, Ap |
| 31 | 396.5 | 23.5 | 14333 | 3 | US-08-781-986A-57 | Sequence 1930, Ap |
| 32 | 395.5 | 23.4 | 924 | 3 | US-09-107-532A-620 | Sequence 227, App |
| 33 | 391 | 23.2 | 1240 | 2 | US-08-869-506-1 | Sequence 424, App |
| 34 | 391 | 23.2 | 1240 | 2 | US-09-128-967-1 | Sequence 563, App |
| 35 | 388 | 23.0 | 995 | 3 | US-09-107-433-2149 | Sequence 1, Appli |
| 36 | 388 | 23.0 | 995 | 3 | US-09-583-110-1930 | Sequence 16264, A |
| 37 | 388 | 23.0 | 5278 | 3 | US-08-961-527-227 | Sequence 1, Appli |
| 38 | 385.5 | 22.8 | 3264 | 3 | US-08-956-171E-424 | Sequence 227, App |
| 39 | 385.5 | 22.8 | 3264 | 3 | US-08-781-986A-424 | Sequence 424, App |
| 40 | 377 | 22.3 | 950 | 3 | US-09-830-230A-563 | Sequence 563, App |
| 41 | 375 | 22.2 | 5449 | 3 | US-09-546-990-1 | Sequence 1, Appli |
| 42 | 374 | 22.2 | 240157 | 3 | US-09-949-016-16264 | Sequence 16264, A |
| 43 | 371 | 22.0 | 1146 | 3 | US-09-711-681-1 | Sequence 1, Appli |
| 44 | 371 | 22.0 | 1146 | 3 | US-10-274-266-1 | Sequence 1, Appli |
| 45 | 371 | 22.0 | 3144 | 3 | US-09-711-681-3 | Sequence 3, Appli |

ALIGNMENTS

RESULT 1

US-08-676-882-1
; Sequence 1, Application US/08676882
; Patent No. 6100241
; GENERAL INFORMATION:
; APPLICANT: Kok, Jacobus Johannes
; APPLICANT: van den Boogaart, Paul
; APPLICANT: Vermeulen, Arnoldus Nicolaas
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 6100241el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,882
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gornley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; TELEFAX: (301) 977-0847
; INFORMATION FOR SEQ ID NO: 1:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1679 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Eimeria acervulina
; DEVELOPMENTAL STAGE: Schizont
; IMMEDIATE SOURCE:
; CLONE: EASC2_1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 280..1269
; OTHER INFORMATION: /function= "Eimeria lactate
; OTHER INFORMATION: dehydrogenase"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..51
; OTHER INFORMATION: /label= pBluescriptII
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1624..1679
; OTHER INFORMATION: /label= pBluescriptII
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 45..54
; OTHER INFORMATION: /label= EcoRI-linker
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1621..1630
; OTHER INFORMATION: /label= EcoRI-linker
;
US-08-676-882-1
Alignment Scores:
Pred. No.: 4,41e-197 Length: 1679
Score: 1688.00 Matches: 330
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-390-846-2 (1-330) x US-08-676-882-1 (1-1679)

Qy 1 MetAlaValPheGluLeuAsnThrArgProLysIleAlaMetValGlySerGlyMetIle 20
Db 280 ATGGCGGCTTCGACAGAATAACACGCCCAAGATTGCTATGGTGGGCTCCGGTATGATT 339

Qy 21 GlyGlyThrMetAlaPheLeuCysSerLeuArgGluLeuGlyAspValValLeuPheAsp 40
Db 340 GGAGGCACCATGGCTTTCCTGTGCAGCTTGAGGGAACCTCGGAGATGTTGTCTCTTCAC 399

Qy 41 ValValProAsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValVal 60
Db 400 GTGTACCGAATCCCGATGGGGAAGCGATGGATATATCGCAAAATCGTCGGTGGTT 459

Qy 61 AspThrGlyIleThrValTyrGlySerAsnSerTyrGluCysLeuLysGlyValAlaAspVal 80
Db 460 GACACGGGTATPAACAGTATACGGCTCAATTCATACAGATGCTTGAAGGGTGGGACGTA 519

Qy 81 ValIleIleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArg 100
Db 520 GTAATAATAACAGCGGATAACAAGATACCCGGAAAGAGCGATAAAGAATGGTCTAGA 579

Qy 101 MetAspLeuLeuProValAsnIleLysIleMetArgGluValGlyAlaAlaIleLysSer 120
Db 580 ATGGATCTATTACCTGTGAATAATAAGATAATAGGGAGGCTCGGTGCAGCAATTAATCT 639

Qy 121 TyrCysProAsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAla 140
Db 640 TACTGCTCTAATGCATTGTTATTATTAATAACAAATCCTTTAGATGTGATGGTAGCTGCT 699

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Qy 141 LeuGlnGluSerSerGlyLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAsp 160
Db 700 CTTCAAGAGTCATCAGGACTACCTCATAGAAATCTCGCGTATCGGTGGGATGCTTGAT 759

Qy 161 SerSerArgPheArgArgMetIleAlaAspLysLeuGluValSerProArgAspValGln 180
Db 760 AGCTCTCGTTTTAGACGTATGATAGCTGATAAATTAGAAAGTCTCTCTCCTAGAGATGTACAG 819

Qy 181 GlyMetValIleGlyValHisGlyAspHisMetValProLeuSerArgTyrAlaThrVal 200
Db 820 GGGATGTCATAGTGTACACGGCGCATCATATGTGCCCCCTAAAGTAGATATGCAACAGTT 879

Qy 201 AsnGlyIleProLeuSerGluPheValLysValLysGlyTrpIleLysGlnGluValAsp 220
Db 880 AAGGCATCCCGCTTCTGAGTTTGTTAAGAGGCTGGATCAAGCAAGAAGAAAGTAGAT 939

Qy 221 AspIleValGlnLysThrLysValAlaGlyGlyLysIleValArgLeuLeuGlyGlnGly 240
Db 940 GATATCGTTCAGAAAGCAAGGTCGCTGGAGGAGAGATCGTACGCCCTATTAGGACAAGGC 999

Qy 241 SerAlaTyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAsp 260
Db 1000 TCTGCTTACTATGCTCCAGGGGCTTCAGCTATTTCAGATGGCTGAGAGCTATCTAAAGGAT 1059

Qy 261 ArgLysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHis 280
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Qy 281 TyrLeuGlyValProCysValIleGlyLysArgGlyValGluLysIleIleGluLeuGlu 300
Db 1120 TACTTAGAGTACCTTGTGTATCGGTGGGAGAGTGTTCAGAAGATTATTAGTTAGAA 1179

Qy 301 LeuThrAlaGlnGluArgGlnGlnLeuGlnGlySerIleAspGluValLysGluMetGln 320
Db 1180 TTGACCGCACAAAGAAAGACAGGAGCTTCAGGGATCTATCGATGAGGTTAAGGAGATCGAG 1239

Qy 321 LysAlaIleAlaAlaLeuAspAlaSerLys 330
Db 1240 AAGGCTATTGCTCTTGTATGCATCCCAAG 1269

RESULT 2
US-09-216-393B-311
; Sequence 311, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhaussen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 311
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Toxoplasma gondii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(75)
; OTHER INFORMATION:
; US-09-216-393B-311

Alignment Scores:
Pred. No.: 1.05e-116 Length: 1785
Score: 1034.50 Matches: 193
Percent Similarity: 77.3% Conservative: 55
Best Local Similarity: 60.1% Mismatches: 72
Query Match: 61.3% Indels: 1
DB: 3 Gaps: 1

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US-09-390-846-2 (1-330) x US-09-216-393B-311 (1-1785)

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QY 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
DB 109 AGAAGAAGTGGCCATGATGGCTCTGGCATGATGGTGACATATGGCTACCTGTGC 168
QY 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
DB 169 GCTCTCCGTGAGCTGCTGACGTGTTCTCTACGATGTTGTCAAAGGTATGCCAGGGT 228
QY 49 LysAlaMetAspIleSerHisAsnSerSerValValAspValValIleThrValTyrGly 68
DB 229 AAGGCTCTGACCTGAGCATGTGACCTCGGTGTCGACCAACGTTTCGGTCCGTGT 288
QY 69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleThrAlaGlyIle 87
DB 289 GAGTACTCTTACGAGCGCGCTACCGTGGCGACTGCTGTTATCGTTACCGCGGTCTG 348
QY 88 ThrLysIleProGlyLysAspLysGluTrpSerArgMetAspLeuLeuProValAsn 107
DB 349 ACCAAGGTGCGGGCAGCCGACTCCGAGTGGAGCCGAAAGCATCTCTCCCGTTCAAC 408
QY 108 IleLysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheVal 127
DB 409 TCGAAGATCATTCGCGAGATCGTCAGAACATCAAGAAGTACTGCCCAAGACCTTCATC 468
QY 128 IleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeu 147
DB 469 ATCGTGGTCCCAACCCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 528
QY 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgArgMet 167
DB 529 CGGACCAACATGATCTCGGTATGCGCTGATGCTGATGCTGATGCTGATGCTGATGCT 588
QY 168 IleAlaPheLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
DB 589 GTCCCGCAGCGGTGTCTGTCTCTCCCGCAGCTGCTGATGCTGATGCTGATGCTGATG 648
QY 188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu 207
DB 649 GCGGACTGTCGGTCCCGCTTGTCCGGTACATTCACCGTGAACGACTACCCCAAGAAC 708
QY 208 PheValLysLysGlyTrpIleLysGlnGluValAspIleValGlnLysThrLys 227
DB 709 TTTCATCAAGGACGCGGTAGTCACGAGNAGCAGCTCGAGGAGATCGCTGACACACCAA 768
QY 228 ValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGly 247

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RESULT 3

US-09-216-393B-313

; Sequence 313, Application US/09216393B

Patent No. 6514694

GENERAL INFORMATION:

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; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 313
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Toxoplasma gondii
US-09-216-393B-313

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Alignment Scores:

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Pred. No.: 1,05e-116 Length: 1785
Score: 1034.50 Matches: 193
Percent Similarity: 77.3% Conservativity: 55
Best Local Similarity: 60.1% Mismatches: 72
Query Match: 61.3% Indels: 1
DB: 3 Gaps: 1

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US-09-390-846-2 (1-330) x US-09-216-393B-313 (1-1785)

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QY 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
DB 109 AGAAGAAGTGGCCATGATGGCTCTGGCATGATGGTGACATATGGCTACCTGTGC 168
QY 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
DB 169 GCTCTCCGTGAGCTGCTGACGTGTTCTCTACGATGTTGTCAAAGGTATGCCAGGGT 228
QY 49 LysAlaMetAspIleSerHisAsnSerSerValValAspValValIleThrValTyrGly 68
DB 229 AAGGCTCTGACCTGAGCATGTGACCTCCGTGGTGCACCAACGTTTCGGTCCGTGCT 288
QY 69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleThrAlaGlyIle 87
DB 289 GAGTACTCTTACGAGCGCGCTACCGTGGCGACTGCTGTTATCGTTACCGCGGTCTG 348
QY 88 ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsn 107
DB 349 ACCAAGGTGCGGGCAGCCGACTCCGAGTGGAGCCGAAAGCATCTCTCCCGTTCAAC 408
QY 108 IleLysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheVal 127
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QY 128 IleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeu 147
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QY 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgArgMet 167
DB 529 CGGACCAACATGATCTCGGTATGCGCTGATGCTGATGCTGATGCTGATGCTGATGCT 588
QY 168 IleAlaPheLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
DB 589 GTCCCGCAGCGGTGTCTGTCTCTCCCGCAGCTGCTGATGCTGATGCTGATGCTGATG 648
QY 188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu 207
DB 649 GCGGACTGTCGGTCCCGCTTGTCCGGTACATTCACCGTGAACGACTACCCCAAGAAC 708
QY 208 PheValLysLysGlyTrpIleLysGlnGluValAspIleValGlnLysThrLys 227
DB 709 TTTCATCAAGGACGCGGTAGTCACGAGNAGCAGCTCGAGGAGATCGCTGACACACCAA 768
QY 228 ValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGly 247

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Db 769 GTGCTGCGCGGAGATCGTCCGCTTCTCGCGCAGGCTTCGGCTTACTACGCCCGCCG 828
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 Db 829 GCATCCGCTGTCCCATCGCAACATCTCTTTGAACGACGAAAGCGCGTCATCCCGTGC 888
 Qy 268 SerCysTyrLeuGlnGlnTyrGlyValGlnAenHisTyrLeuGlyValProCysVal 287
 Db 889 AGTGTGTACTGCAACGAGAGTACGGCTTGAGGACATGTTCAATGTGTCTCCCGCGCTC 948
 Qy 288 IleGlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGln 307
 Db 949 ATTGAGGCGCGGCGCATCGAGCGCTCATCGAGCTCGAGCTGAAACGAGGAGGAGAAG 1008
 Qy 308 GluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaIleuAsp 327
 Db 1009 CAGTTCAGAGATCGCTCGACGACGTATCGGCTCAACAAGCGGCTGTCTCTTCAG 1068
 Qy 328 Ala 328
 Db 1069 GCG 1071

RESULT 4

PCT-US94-03796-1

; Sequence 1, Application PC/TUS9403796

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: GENE ENCODING THE LACTATE DEHYDROGENASE

; NUMBER OF SEQUENCES: 15

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/03796

; FILING DATE: 06-APR-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/046,160

; FILING DATE: 12-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Deconti, Giulio A.

; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: DCI-066CPPC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 951 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..945

PCT-US94-03796-1

Alignment Scores:

Pred. No.:

Score: 3.43e-92

Length: 951

Matches: 167

Conservative: 51

Mismatch: 95

Indels: 3

Gaps: 2

US-09-390-846-2 (1-330) x PCT-US94-03796-1 (1-951)

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Db 10 AAAGCAAAAATCGTTTGTAGTTGGCTCAGGTATGATTGGAGGAGTAATGGCTACCTTAATT 69
 Qy 29 SerLeuArgGluLeuGlyAspValValIleuPheAspValValProAenMetProMetGly 48
 Db 70 GTTCAGAAAAATTTAGGAGATAGTATTGTTTGCATATTGTAAGAAACATGCCACATGGA 129
 Qy 49 LysAlaMetAspIleSerHisAenSerSerValValAspThrGlyIleThrValTyrGly 68
 Db 130 AAAGCTTTAGTACATCTCATCTAATGTTATGGCATATTCAAATTCGCAAGTAAGTGGT 189
 Qy 69 SerAenSerTyrGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr 88
 Db 190 TCAACACTTATGACGATTGCTGGAGCAGATGTAATAGTAATAGTAACAGCTGGATTACC 249
 Qy 89 LysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsnIle 108
 Db 250 AAGCCCCAGGAAAGAGTGACAAAGATGGAATAGAGATGATTATTATCCATTAAACAAC 309
 Qy 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAenAlaPheValIle 128
 Db 310 AAGATTATGATTGAATGTTGGTGCATATTAGAGAAATGTCCTCAATGCTTTTATTATT 369
 Qy 129 AsnIleThrAenProLeuAspValMetValAlaAlaLeuGlnGlnLysSerSerGlyLeuPro 148
 Db 370 GTTGTAAACAAACCCAGTAGATGTTATGGTACAAATTATTACATCAACATTCAGGTGTTCT 429
 Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMetIle 168
 Db 430 AAAAACAAGATTATGTTAGGTGGTATTAGATACATCAAGATTGAAGATTGAAGATTACATA 489
 Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
 Db 490 TCTCAGAAATTAATGATGCCCAAGAGATGTAATGCCACACATTTGAGGTGCTCATGGA 549
 Qy 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe 208
 Db 550 AATAAAATGTTCTTTTAAAAAGATACATTTACTGTAGGTGTTCCCTTTTACAAGAAATTT 609
 Qy 209 ValLysLysGlyTrpIleLysGlnGluValAspAspIleValGlnLysThrLysVal 228
 Db 610 ATTAATAACAAGTTAATTTCTGATGCTGAATTAGAAGCTATATTTGTAGAAGCTGTTAAT 669
 Qy 229 AlaGlyGlyGluIleValArgLeuGlyGlnGlySerAlaTyrTyrAlaProGlyVala 248
 Db 670 ACTGCATTAGAAATGTAACCTTA-----CATGCATCACCATATGTGCACAGCTGCT 723
 Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
 Db 724 GCTATTATCGAAATGGCTGAATCCTACTTAAAGATTGAAAAAAGTATTAAATTTGCTCA 783
 Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
 Db 784 ACCTTGTTAGAAGGACAATATGGACACTCCGATATATTTCGGTGGTACACCTGTTGTTT 843
 Qy 289 GlyGlyArgGlyValGluLysIleIleGluLeuLeuThrAlaGlnGlnArgGlnGlu 308
 Db 844 GGTCTAATGTTGTTGAACAGTTATCGAATTCAATTAAATAGTAGAGAAAAAGCTAAA 903
 Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAla 324
 Db 904 TTTGATGAAGCCATAGCTGAAGAACTAAGAGAATG--AAGGCATTAGCT 948

RESULT 5

US-08-270-013B-1

; Sequence 1, Application US/08270013B

; Patent No. 5686294

; GENERAL INFORMATION:

; APPLICANT: Sogabe et al.

; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE

; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.

127 ValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerGly 146
1040 ATCATCGTCTTGACGAACCGGTCGATCGCATGACGTATACGGTCTTTAAGGAATCCGGA 1099
147 LeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArg 166
1100 TTCCCGAANAACCGCGTCATCGGCCAGTCGGCGGTCTTGATATACGGCGCGCTTCCGACG 1159
167 MetIleAlaAspIysLeuGluValSerProArgAspValGlnGlyMetValIleGlyVal 186
1160 TTCGTGCCGAGAGCTGAACATTTGGTAAAGATGTCACTGGGTGTGTTTAGCGCGC 1219
187 HisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSer 206
1220 CATGGCGATGACATGTCGCGCTCGTCCGCTACTCGTACGCCGCGGCATTCGCTCGAA 1279
207 GlupheValIysGlyTrpIleIysGlnGluValAspAspIleValGlnIysThr 226
1280 AAATCATTCGGA-----GATCGTTTGGACGCCATCGTTGAGCGGACG 1324
227 LysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaPro 246
1325 CGCAAGGGCGCGGTGAATCTGCTCACTGCTCGGCAACGGCAGCGCTACTACGACCG 1384
247 GlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetVal 266
1385 GCCGCTCGCTTCTCGAAATGGTCGAAGCGATTTTCAAAGACCAGCGCCGCAATTTGCGC 1444
267 CysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCys 286
1445 GCGATCGCTTACCTTGAAGCGGAATACGGCTATGAAGGCATTTATTTGGCGGTGCGGACG 1504
287 ValIleGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArg 306
1505 ATCTCGGGCGCAACGGCATCGAAGAATGATCGACTCGAGCTGACCTGACCGAAGAGGAAAA 1564
307 GlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIle 323
1565 GC-GCGCTCGCCAATCCGTGCAATCCGTTAAAAATGTCATGCGCATCGTG 1614

RESULT 6
US-08-838-418-1
; Sequence 1, Application US/08838418
; Patent No. 5744342
; GENERAL INFORMATION:
; APPLICANT: Sorabe et al.
; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601-6780
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,418
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/270,013
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 164701/1993
; FILING DATE: 02-JUL-1993
; ATTORNEY/AGENT INFORMATION:

Db 1280 AAACCTCATTCGAAA-----GATCGTTTGGACGCCCACTGTTTAGCGGCAGC 133
 QY 227 LysValAlaGlyGlyGluIleValArgLeuGlyGlnGlySerAlaTyrTyrAlaPro 246
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1325 CGCAAAAGGCGCGGTGAATACTGTCACACTGCTCGGCNACCGCACGCGCTACTACGCACCG 138
 QY 247 GlyAlaserAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetVal 266
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1385 GCGCGCTCGCTGTCGAAATGTCGAAGCGGATTTTGNAAGACCAGCGCGCATTTTGGCGGTCCGACG 144
 QY 267 CysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCys 286
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1445 GCGATCGCCTACCTTGAAGCGCAATACGGCTATGAAGGCATTTATTATTGGCGGTCCGACG 150
 QY 287 ValIleGlyGlyArgGlyValGluLysIleIleGluLeuLuleuThrAlaGlnGluArg 306
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1505 ATCCTCGGCGGCACCGCATCGAGAAAGTGATCGAGCTCGAGCTGACCGAAGAGGGA AAAA 156
 QY 307 GlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIle 323
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1565 GC-GCGCTCGCCAAATCCGTCGAATCCGTTAAAAATGTCATGCGCATCGTG 1614

RESULT 7
 US-09-902-540-6244
 ; Sequence 6244, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902.540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 6244
 ; LENGTH: 870
 ; TYPE: DNA
 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-6244

| Alignment Scores: | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 2.37e-75 | Length: | 870 |
| Score: | 694.00 | Matches: | 140 |
| Percent Similarity: | 66.8% | Conservative: | 59 |
| Best Local Similarity: | 47.0% | Mismatches: | 87 |
| Query Match: | 41.1% | Indels: | 12 |
| DB: | 3 | Gaps: | 3 |

US-09-390-846-2 (1-330) X US-09-902-540-6244 (1-870)
 QY 6 LysAsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAla 25
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 7 CAGAATGGCAAGAAGATCGGCTCATCGCGCGCGTCCAGATCGCGCGCAACCTGGCG 66
 QY 26 PheLeuCysSerLeuArgGluLeuGlyAspValValLuuPheAspVal-----ValPro 43
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 67 CTGCTCGCCGTCGCAAGATCGCTCGGTGACGTGTGTACGACATCCCGCGCGCCGAG 126
 QY 44 AsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValValAspThrGly 63
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 127 GGTCTGTCGAAGGCAAGGCGCTGCAATCAACAGCTGGCGCGGTTCGCGTTACGAC 186
 QY 64 IleThrValTyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValllleIle 83
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 187 TGCCGCGTGAAGGCAACCGCATCGGAGAACGTGGCTGGCTCGGACGTGATCATCATC 246
 QY 84 ThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeu 103
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 247 ACGGCCGCGCATGCCCGCAAGCGCGG-----ATGTCGCGGAGGACCTG 291

| | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|-----|---------|----------|--------|--------|--------|-------|-------|--------|---------|----------|--------|--------|-------|------|-----------|------|-------|------------|-----|------|-----|
| QY | 6 | LYS | ASNT | ARG | PRO | LYS | ILE | ALA | MET | VAL | GLY | SER | GLY | MET | ILE | GLY | THR | MET | ALA | 25 | | | |
| DB | 866 | CAG | AT | TGG | CAG | AA | AAG | AT | CGG | CT | CAT | CGC | CGC | GGT | CAG | AT | CGC | CGC | CAAC | CTGGCG | 807 | | |
| QY | 26 | PH | LEU | CYS | SER | LEU | ARG | GLU | LEU | CYS | LYS | ASP | VAL | VAL | LEU | PH | EAS | PVAL | ----- | VAL | PRO | 43 | |
| DB | 806 | CTG | CT | CGC | GTG | CAG | AAT | CGC | T | CGG | T | GAC | TGT | G | TGT | TAC | GCA | CAT | CCCG | CGCGCGCGAG | 747 | | |
| QY | 44 | ASN | MET | PRO | MET | GLY | LYS | ALA | MET | ASP | ILE | SER | HIS | ASN | SER | VAL | VAL | ASP | THR | GLY | 63 | | |
| DB | 746 | G | TCT | TGG | T | CAG | GCA | AGC | CGC | T | GCA | CAT | CA | CAC | AGC | TGG | CGCGCGGTG | CGGT | TAC | CGGT | TAC | GCAC | 687 |
| QY | 64 | ILE | THR | VAL | TYR | GLY | SER | ASN | SER | TYR | GLU | CYS | LEU | LYS | GLY | ALA | ASP | VAL | ILE | ILE | 83 | | |
| DB | 686 | TCC | CGCGGT | GAA | GGG | CAC | CGA | CTG | GAA | GAG | CGT | TGC | T | GGC | T | CGG | ACG | GTG | GAT | CAT | CAT | 627 | |
| QY | 84 | THR | ALA | GLY | ILE | THR | LYS | ILE | PRO | GLY | SER | ASP | LYS | GLU | TRP | SER | ARG | MET | ASP | LEU | 103 | | |
| DB | 626 | ACG | CGCGCAT | TGCCCCCG | CAAC | CGGGC | ----- | ATG | TCCCG | CGAGG | ACCTG | 582 | | | | | | | | | | | |
| QY | 104 | LEU | PRO | VAL | ASN | ILE | LYS | ILE | MET | ARG | GLU | VAL | GLY | ALA | ALA | ILE | LYS | SER | TYR | CYS | PRO | 123 | |
| DB | 581 | CTC | GAG | ATCA | CACT | GAA | GAT | CAT | GAC | GAG | TGG | CGGGCAAC | ATCAAG | CAG | CAG | ACG | CCCCC | 522 | | | | | |
| QY | 124 | ASN | ALA | PH | VAL | ILE | ASN | ILE | THR | ASN | PRO | LEU | ASP | VAL | MET | VAL | ALA | ALA | LEU | GLN | 143 | | |
| DB | 521 | AAC | GCTT | CGT | CAT | CAAG | CTG | CCCA | CCCG | CTG | GAC | CGG | ATG | T | TTC | GGC | CTCC | CAAG | 462 | | | | |
| QY | 144 | SER | SER | GLY | LEU | PRO | HIS | HIS | ARG | ILE | CYS | GLY | MET | ALA | GLY | MET | LEU | ASP | SER | SER | ARG | 163 | |
| DB | 461 | AT | CGCGCGT | CTCTCG | CCCA | GAC | CA | TG | TGT | CGCGGG | CAT | GGCGGG | CTGT | GGAC | CGTGT | GGAC | ACAC | CAG | CGCG | 402 | | | |
| QY | 164 | PH | E | ARG | ARG | MET | ILE | ALA | ASP | LYS | LEU | GLU | VAL | SER | PRO | ARG | ASP | VAL | GLN | GLY | MET | VAL | 183 |
| DB | 401 | TTC | AAG | TGCTTC | GTG | CGCGAG | CGCCT | GGGT | GTCT | TCCAT | CGCCAC | GTGGAGG | CCCC | CTGGTG | 342 | | | | | | | | |
| QY | 184 | ILE | GLY | VAL | HIS | GLY | ASP | HIS | MET | VAL | PRO | LEU | SER | ARG | TYR | ALA | THR | VAL | ASN | GLY | ILE | 203 | |
| DB | 341 | CTG | GGCGG | CCAC | GGG | GAC | GAC | ATG | T | CCCG | CTGT | CGGCC | CAC | AGG | AC | GGT | GGCGCG | CGTG | 282 | | | | |
| QY | 204 | PRO | LEU | SER | GLU | PH | E | VAL | LYS | GLY | TRP | ILE | LYS | GLN | GLU | VAL | ASP | ASP | ILE | VAL | 223 | | |
| DB | 281 | CCC | CTG | ACG | GAG | TGAT | CGCC | CAAG | ----- | GACA | AGT | GTG | GAC | GCGCAT | CAT | CAT | C | 237 | | | | | |
| QY | 224 | GLN | LYS | THR | LYS | VAL | ALA | GLY | GLY | GLU | ILE | VAL | ARG | LEU | LEU | GLY | GLN | GLY | SER | ALA | TYR | 243 | |
| DB | 236 | AAG | CGCAC | CCCG | GTG | AGG | CGCGCG | CGG | AGC | TGT | CGT | CTG | TAC | AAG | ACG | CGG | CAG | CGC | TAC | 177 | | | |
| QY | 244 | TYR | ALA | PRO | GLY | ALA | SER | ALA | ILE | GLN | MET | ALA | GLU | SER | TYR | LEU | LYS | ASP | ARG | LYS | ARG | 263 | |
| DB | 176 | TTC | GGCCCCG | GGGTG | CGCAT | CCCAT | GGCGAG | AGCTT | CTG | CAG | GAC | CGC | AGCG | CTAC | 117 | | | | | | | | |
| QY | 264 | VAL | MET | VAL | CYS | SER | CYS | TYR | LEU | GLN | GLY | TRP | GLY | VAL | GLN | ASN | HIS | TYR | LEU | GLY | 283 | | |
| DB | 116 | GTG | TG | CGCGCG | CGCCCT | CTCTGG | AGGGCC | AGTAC | GGGAT | CAAC | CGGTACT | CTCT | TCTGCG | 57 | | | | | | | | | |
| QY | 284 | VAL | PRO | CYS | | | | | | | | | | | | | | | | | | | |

[illegible]

DEC 11 1966

US-09/134-001C-2696
; Sequence 2696, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: LYNN DOUCETTE-STAMM ET AL
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08

; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08

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; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2696
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2696

Alignment Scores:
Pred. No.: 9 37e-69 Length: 978
Score: 641.00 Matches: 132
Percent Similarity: 64.0% Conservative: 71
Best Local Similarity: 41.6% Mismatches: 102
Query Match: 38.0% Indels: 12
DB: 3 Gaps: 4

US-09-390-846-2 (1-330) x US-09-134-001C-2696 (1-978)
Qy 9 ArgProlylIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 46 AGAAGAAAGATATCAATATTATGGCGCGGCACATACAGGTGGGACTCTAGCATTCATTCTT 105
Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAsp-----ValValProAsnMetPro 46
Db 106 GCACAAAAGGAATAGGAGATATTGTGTGATTGAACGCCAGCAATCAGAGGGTATGGCT 165
Qy 47 MetGlyLysAlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrVal 66
Db 166 AAAGAAAGGGTTAGATATTATTTAGAAAGCGGCCCATTTGGGGTTTGACACATCTGTA 225
Qy 67 TyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleIleThrAlaGly 86
Db 256 CATGTTTCAGTAAATATAGAGATATTAAAGATTACAGACATAGTGGTGCATGACGCAGGT 285
Qy 87 IleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProVal 106
Db 286 -----ATACCTTAGGAATCAGGA-----ATGCAAGAGAAAGAAATTAGTTCAAACT 330
Qy 107 AsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPhe 126
Db 331 AATGACAAATAGTACGAGAACTGCATTACAAATTCGACGTATGCACCTCATTCATA 390
Qy 127 ValIleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGly 146
Db 391 ATTATTGTATTGACTAATCCGGTTGATGTATGACATATCTGCTATTTAAAGCATCAGGT 450
Qy 147 LeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArg 166
Db 451 TTTCTTAAGAACGTTATTATTGGTCAATCTGGAATTTTAGACGCTGCAAGATATCGAAT 510
Qy 167 MetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyVal 186
Db 511 TTTATTGCTCAGAACTTAACGTGCTGTCGCAAGATGTAATGGGTTGTTTAGTGA 570
Qy 187 HisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSer 206
Db 571 CATGGTGATACGATGTACCTTTGATTGATTAATACACACATTAATGGGATCCAGTT--- 627
Qy 207 GluPheValLysGlyTrpIleLysGlnGluValAspAspIleValGlnLysThr 226
Db 628 -----AAGCATCTTATTTCTGAAGAAAGATTTGATCAATATTTGTAAGCTACA 675
Qy 227 LysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaPro 246
Db 676 CTAAGGGTGGTGCAGAAATTTGTCATTACTAGTCAAGGCTCAGCATATTATGCACCA 735
Qy 247 GlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgGlyArgValMetVal 266
Db 736 GCAACTGCTATATATGAACTATAGATGCAATTTTAAATGATCGGAAACGGTTATTACCA 795
Qy 267 CysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCys 286
Db 267 CysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCys 286

; PRIOR APPLICATION NUMBER: US 08/920,812
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2696
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2696

Alignment Scores:
Pred. No.: 9 37e-69 Length: 978
Score: 641.00 Matches: 132
Percent Similarity: 64.0% Conservative: 71
Best Local Similarity: 41.6% Mismatches: 102
Query Match: 38.0% Indels: 12
DB: 3 Gaps: 4

US-09-390-846-2 (1-330) x US-08-920-812-7 (1-5024)
Qy 9 ArgProlylIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 57 AGAAGAAAGATATCAATATTATGGCGCGGCACATACAGGTGGGACTCTAGCATTCATTCTT 116
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Db 402 AATTATTGTTGACTAATCGGTGATGTTATGACATATATCTGCAATTTAAAGCATCAGG 461
Qy 146 YLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerArgPheArgAr 166
Db 462 TTTTCTAAAGAACGCTATTATTGTTGCTCAATCTGGAATTTTAGACGCTGCAAGATATCGAAC 521
Qy 166 gMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyVa 186
Db 522 TTTTATTGCTCAAGAACTTAACGTGCTGTCARAGATGTAATGCGTTGTTTATTAGGTGG 581
Qy 186 lHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSe 206
Db 582 ACATGGTGATACGATGTTACCTTTGATTAATAACACACACATTAATGGATTCAGATT-- 639
Qy 206 rGluPheValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysTh 226
Db 640 -----AAGCATCTTATTCTGAAGAAAGATTGATCAAAATTGTTGAACGTAC 686
Qy 226 rLysValAlaGlyGlyIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaPr 246
Db 687 ACGTAAAGGTGGTCAGAAATTTGTCATTACTAGTCACGCTCAGCATATTATGACCC 746
Qy 246 oGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetVa 266
Db 747 AGCAACTCTATATATGAACACTATAGATGCAATTTTAAATGATCGGAACGGTTATTACC 806
Qy 266 lCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCy 286
Db 807 AAGTATTGCTTATCTAGAGGAGAAATACGGTTGTTGACATATTGTTTCCGAGTTCCTAC 866
Qy 286 sValIleGlyGlyArgGlyValGluValIleGlyLeuGluLeuThrAlaGlnGluAr 306
Db 867 TATTAATAGATATCAAGGAATAGAAAGATATTAGAGTAGATATGAATAATGATGAGTA 926
Qy 306 gGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIle 323
Db 927 TCACAACTACACACTCTCGCGCAAGATGTGAGTGAAGTCAAAACTCACTA 978

RESULT 12
US-08-921-177-7
; Sequence 7, Application US/08921177
; Patent No. 5798211
; GENERAL INFORMATION:
; APPLICANT: Chono, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921.177
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
US-08-921-177-7

Alignment Scores: 1.65e-66 Length: 5024
Pred. No.: 632.00 Matches: 132
Score: 64.2% Conservative: 72
Best Local Similarity: 41.5% Mismatches: 101
Query Match: 37.4% Indels: 13
DB: 2 Gaps: 4

US-09-390-846-2 (1-330) x US-08-921-177-7 (1-5024)

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 57 AGAAGAAAGATATCAATTTATTTGGCGGGACATACAGGTGGGACTCTAGCATTCATTCTT 116
Qy 29 SerLeuArgGluLeuGlyAspValValPheAsp-----ValValProAsnMetPro 46
Db 117 GCACAAAGGAATTAGAGATATTGTTGATTGAACGCCAGCAGCATCAGGGGTATGGCT 176
Qy 47 MetGlyLysAlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrVal 66
Db 177 AAAGAAAGCGGTAGATATTTTAGAAAGCGGACCCATTTGGGGGTTTGCACATCTGTA 236
Qy 67 TyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValIleIleThrAlaGly 86
Db 237 CATGGTTTCAGTAAATATAGAGATATTAAAGATTCACACATAGTGGTGATGACTGCAGGT 296
Qy 87 IleThrLysIleProGlyLysSerAspLysGluTyrSerArgMet-AspLeuLeuProVa 106
Db 297 -----ATACCTAGGAATCAGGA-----ATGACAGGAGAGAAGATTTAGTCAAC 341
Qy 106 lAsnIleLysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPh 126
Db 342 TAATGAACAAATAGTACGAGAACTGCATTACAAATTTGCAACGATATGCACCTCATTCAAT 401
Qy 126 eValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGl 146
Db 402 AATTATTGTTATGACTAATCCGTTGATGTTATGACATATATCTGATTTAAAGCATCAGG 461
Qy 146 YLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerArgPheArgAr 166
Db 462 TTTTCTAAAGAACGCTATTATTGTTGCTCAATCTGGAATTTTAGACGCTGCAAGATATCGAAC 521
Qy 166 gMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyVa 186
Db 522 TTTTATTGCTCAAGAACTTAACGTGCTGTCARAGATGTAATGCGTTGTTTATTAGGTGG 581
Qy 186 lHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSe 206
Db 582 ACATGGTGATACGATGTTACCTTTGATTAATAACACACACATTAATGGGATTCAGATT-- 639
Qy 206 rGluPheValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysTh 226
Db 640 -----AAGCATCTTATTCTGAAGAAAGATTGATCAAAATTGTTGAACGTAC 686
Qy 226 rLysValAlaGlyGlyIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaPr 246
Db 687 ACGTAAAGGTGGTCAGAAATTTGTCATTACTAGTCACGCTCAGCATATTATGACCC 746
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| | | | |
|----|-----|---|-----|
| Qy | 246 | oGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetVa | 266 |
| | | :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: | |
| Db | 747 | AGCAACTGCTATATATGAACCTATAGATGCATTTTAAATGATCGAAACGGTTATTACC | 806 |
| Qy | 266 | lCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCy | 286 |
| Db | 807 | AAGTATTGCTTATCTAGAGGGAGAATAACGGTTGTTCAGATATTCTGTCGGAGTTCCTAC | 866 |
| Qy | 286 | sValIleGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluAr | 306 |
| Db | 867 | TATAATAGGATATCAAGGAATAGAAAAGATTATAGAGGTAGATATGAATATATGATGAGTA | 926 |
| Qy | 306 | gGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIle | 323 |
| Db | 927 | TCACAACACTCAACACTCTGCCAAGATGTGAGTGAAGTCAAAAACTCACTA | 978 |

RESULT 13

US-08-362-577C-7
; Sequence 7, Application US/08362577C
; Patent No. 5807673
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsunisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

| | | |
|------------------------|----------|---------------|
| Alignment Scores: | | |
| Pred. No.: | 1.65e-66 | Length: |
| Score: | 632.00 | Matches: |
| Percent Similarity: | 64.2% | Conservative: |
| Best Local Similarity: | 41.5% | Mismatches: |
| Query Match: | 37.4% | Indels: |
| DB: | 2 | Gaps: |
| | | 4 |
| | | 5024 |

US-09-390-846-2 (1-330) x US-08-362-577C-7 (1-5024)

| | | | | | | | | | | | | |
|----|-----|---------|----------|--------------|----------|---------|---------|---------|--------|--------|---------|-----|
| Qy | 9 | ArgPro | Ys | IleAlaMetVal | GlySer | GlyMet | IleGly | GlyThr | MetAla | PheLeu | Cys | 28 |
| Db | 57 | AGAAGA | AGATAT | CAATTT | TATTTG | CGCGGAC | CATACAG | GTGGAC | TCTAG | CATTCA | TTCTTT | 116 |
| Qy | 29 | SerLeu | ArgGlu | LeuGly | AspVal | ValLeu | PheAsp | ----- | ValVal | ProAsn | MetPro | 46 |
| Db | 117 | GCACAA | AAAGGA | TAATAG | GAGATATT | TGTGTG | TGTAAT | GAAACG | CCAGCA | ATACAG | GGGTAT | 176 |
| Qy | 47 | MetGly | YsAlaMet | AspIle | SerHis | AsnSer | SerVal | ValAsp | ThrGly | IleThr | Val | 66 |
| Db | 177 | AAAGAA | AGCGGT | TAGATAT | TTT | TAGA | AAACG | CCCATTT | TGGGGT | TTGCAC | NCACTCT | 236 |
| Qy | 67 | TyrGly | SerAsn | SerTyr | GluCys | LeuGly | AlaAsp | ValVal | IleIle | ThrAla | Gly | 86 |
| Db | 237 | CATGGT | TCAGTAA | TATAGA | AGATATT | AAAGATT | CAGACA | TAGTGG | TGTCAT | GACTG | CAGCT | 296 |
| Qy | 87 | IleThr | lysIle | ProGly | YsSer | AspIys | GluTrp | SerArg | Met | AspLeu | LeuPro | 106 |
| Db | 297 | ----- | ATAC | CTAG | GAATC | AGGA | ----- | ATGCA | AGGAG | AAAGTA | TAGTTCA | 341 |
| Qy | 106 | LAsn | IleLys | IleMet | ArgGlu | ValGly | AlaAla | IleLys | SerTyr | CysPro | AsnAla | 126 |
| Db | 342 | TAATG | ACAATA | TAGTAC | GAGAA | CTGCAT | TACA | ATTG | CAACGT | TGCAC | CTCAT | 401 |
| Qy | 126 | eVal | IleAsn | IleThr | AsnPro | LeuAsp | ValMet | ValAla | AlaLeu | GlnGlu | SerSer | 146 |
| Db | 402 | AAATTAT | TGTTG | TAATC | CGGTTG | TGATG | TTATG | CACAT | TATACT | GCATTA | TCTAA | 461 |
| Qy | 146 | YLeu | ProHis | IleArg | IleCys | GlyMet | AlaGly | MetLeu | AspSer | SerArg | PheArg | 166 |
| Db | 462 | TTTTCT | TAAAGA | ACGTAT | TATG | TGCTCA | ATTG | TGSA | ATT | TTAG | COC | 521 |
| Qy | 166 | gMet | IleAla | AspIys | LeuGlu | ValSer | ProArg | AspVal | GlnGly | MetVal | IleGly | 186 |
| Db | 522 | TTTTAT | TGCTCA | GAAC | CTTA | ACGTG | CTGCTG | CAAGA | GTAA | TATGG | TTT | 581 |
| Qy | 186 | LHis | GlyAsp | HisMet | ValPro | LeuSer | ArgTyr | AlaThr | ValAla | GlnIle | ProLeu | 206 |
| Db | 582 | ACATGG | TGATAC | GAATG | TATAC | CTTTG | ATTA | ATAA | CAAC | ACATTA | TATGG | 639 |
| Qy | 206 | rGlu | PheVal | lysIys | GlyTrp | IleLys | GlnGlu | ValAsp | PheIle | ValGln | LysTh | 226 |
| Db | 640 | ----- | AAGCA | TCTTAT | TTCTG | GAAGAA | AAGATT | GATCAA | AATG | TGTTG | TGAAC | 686 |
| Qy | 226 | rLys | ValAla | GlyGly | GluIle | ValArg | LeuLeu | GlyGln | GlySer | AlaTyr | IleAla | 246 |
| Db | 687 | ACGTA | AGGTGT | GCAGAA | TTGTTG | CACTACT | AGGCTCA | AGGCTC | GACAT | TATATG | CAAC | 746 |
| Qy | 246 | oGly | AlaSer | AlaIle | GlnMet | AlaGlu | SerTyr | LeuLys | AspArg | IysArg | ValMet | 266 |
| Db | 747 | AGCAAC | TGCTAT | TATG | AAACTA | PAGATG | CAAA | TTTT | TAAT | GATCGG | AAACG | 806 |
| Qy | 266 | lCys | SerCys | TyrLeu | GlnGly | GlnTyr | GlyVal | GlnAsn | HisTyr | LeuGly | ValPro | 286 |
| Db | 807 | AAGTAT | TGCTTAT | CTAGG | GAGAA | TACGGT | TGTT | TCAGAT | TATTTG | TTTCG | GAGTTC | 866 |
| Qy | 286 | sVal | IleGly | GlyArg | GlyVal | GluLys | IleIle | GluLeu | GluLeu | ThrAla | GlnGlu | 306 |
| Db | 867 | TATAAT | TAGGAT | ATCA | AGGA | TAGAA | ATTAT | GAGGT | AGAT | TATGA | TATATG | 926 |
| Qy | 306 | gGln | GluLeu | GlnGly | SerIle | AspGlu | ValLys | GluMet | GlnLys | AlaIle | 323 | |
| Db | 927 | TCAACT | AACTACA | CACTCT | CGCA | AGATG | TGCA | GTG | GAAGT | CAAA | AACTCA | 978 |

RESULT 14

RESUME 14
US-08-920-828-7
; Sequence 7, Application US/08920828
; Patent No. 5853998
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu

; APPLICANT: Eda, Soji
 ; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/920,828
 ; FILING DATE: 29-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/362,577
 ; FILING DATE: 27-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 19036/32420
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5024 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Staphylococcus epidermidis
 ; STRAIN: Clinical Isolate SE-32
 ; US-08-920-828-7

Alignment Scores:
 Pred. No.: 1,658-66 Length: 5024
 Score: 632.00 Matches: 132
 Percent Similarity: 64.2% Conservative: 72
 Best Local Similarity: 41.5% Mismatches: 101
 Query Match: 37.4% Indels: 13
 DB: 2 Gaps: 4

US-09-390-846-2 (1-330) x US-08-920-828-7 (1-5024)

Qy 9 ArgProLysAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
 Db 57 AGAAGAGATATCAATATTGCGCGGCACATACAGTGGGACTTAGCATTCTT 116
 Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAsp-----ValValProAsnMetPro 46
 Db 117 GCACAAAGGAATATTAGGAGATATTGTTGATTGAAGCCGACCAATCAGAGGGTATGGCT 176
 Qy 47 MetGlyLysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrVal 66
 Db 177 AAGAGAAAGCGCTTAGATATTAGAAAGCGGACCCATTGGGGGTTTGACACATCTGTA 236
 Qy 67 TyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleThrAlaGly 86
 Db 237 CATGGTTCAGTAATATAGAAAGATATTAAAGATTAGACATAGTGGTGTAGTCCAGGT 296
 Qy 87 IleThrLysIleProGlyLysSerAspLysGluTrpSerArgMet-AspLeuLeuProVa 106
 Db 297 -----ATACCTAGGAATCAGGA-----ATGCAAGGAGGAAGAAATTAGTTCAAAC 341
 Qy 106 IAsnIleLysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPh 126

Db 342 TAATGAACAATAGTACGAGAACTGCATTACAAATTTGCAACGTATGCACCTCATTCAT 401
 Qy 126 eValIleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGly 146
 Db 402 AATTATTGTTATGACTAATCCGGTTGATGTTATGACATATATGTCATTTAAAGATCAGG 461
 Qy 146 YLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgAr 166
 Db 462 TTTTCCTAAAGAACGTATTATTGTCATCTGGAAATTTAGACCTCGAAGATATCGAAC 521
 Qy 166 gMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyVa 186
 Db 522 TTTTATTGCTCAAGAACTTAACGTGCTGTCAGAGATGTAATGGTTGTTTGTAGGTGG 581
 Qy 186 lHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSe 206
 Db 582 ACATGGTGATACGATGTTACCTTTGATTAAATAACACACACACATTAATGGGATTCAGTT-- 639
 Qy 206 rGluPheValLysGlyTrpIleLysGlnGluValAspAspIleValGlnLysTh 226
 Db 640 -----AAGCATCTTATTTCTGAAGAAAGATGATCAAAATTGTTGACGTAC 686
 Qy 226 rLysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerIleTyrAlaPr 246
 Db 687 ACGTAAAGGGTGGTCAGAAATTTGTCATTACTAGGTCAAGGCTCAGCATATTATGCACC 746
 Qy 246 oGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetVa 266
 Db 747 AGCAACTGCTATATATGAACTATAGATGCAATTTTAAATGATCGGAACGGTTATTACC 806
 Qy 266 lCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCy 286
 Db 807 AAGTATTGCTTATCTAGGAGGAATACGGTTGTTTCAGATATTGTTTCGAGGTTCTCTAC 866
 Qy 286 sValIleGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluAr 306
 Db 867 TATAATAGGATATCAAGGAATAGAAAGATTATAGAGGTAGATATGAATAATGATGACTA 926
 Qy 306 gGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIle 323
 Db 927 TCAACAACACTACACACTCTGCGCAAGATGTGAGTGAAGTCAAACTCACTCACTA 978

RESULT 15
 US-09-107-532A-2832
 ; Sequence 2832, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660
 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107,532A
 ; FILING DATE: 30-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085,598
 ; FILING DATE: 14 May 1998
 ; APPLICATION NUMBER: 60/051571
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:

```

202 GlyIleProLeuSerGluPheValIysLysGlyTrp---IleLysGlnGluGluValAsp 220
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
607 GGTAAACAGGTCTTTTGAATTTGTAGAAAAGACCATCGTATTGCCAAGATGAATTAGAT 666
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

221 AspIleValGlnLysThrLysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGly 240
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
667 GTGATTGCTGATAAAGTCGTAAGTCGCTTATGAGATCAATTGAT-----CGTAAAAA 720

241 SerAlaTyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAsp 260
    ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
721 GCAACTTACTATGTTGTTGTTGATGAGTACTGCACGTATCGTAAAGCATCTCTTGAATAAC 780

261 ArgLysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHis 280
    ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
781 GAACAGCTGTATTCCCTGTATTCCTGTTATTTAACTGGTGAATACGACGAAAAGATATC 840

281 TyrLeuGlyValProCysValIleGlyIArgGlyValGluLysIleIleGluLeuGlu 300
    ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
841 TTTACAGGTGTGCCATCAATCGTTGACGAAAATGTTGTCGTGAAGTTGTTGAATTATCA 900

301 LeuThrAlaGlnGluArgGlnGluLeuGlnGlySerIleaspGluLysGluMetGln 320
    ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
901 ATCAACGAAGAAGRAAAAAGCAATCTTCAGCAAAATCAACAGTCTCTTAAAGAGAAGTATTG 960

321 LysAlaIle 323
    ::::
961 AACACTGTA 969

```

US-09-390-846-2 (1-330) x US-09-107-532A-2832 (1-975)

| | | | |
|----|-----|--|-----|
| Qy | 3 | ValPheGluLysAsnThrArgProLysIleAlaMetValGlySerGlyMetIleGlyGly | 22 |
| Db | 25 | TTATTCATGAAAAAACAAAGTCGTAAGACTAGTAATCGTCGTACAGCTTTGTGTGGAACA | 84 |
| Qy | 23 | ThrMetAlaPheLeuCysSerLeuArgGluLeu---GlyAspValValIleuPheAspVal | 41 |
| Db | 85 | AGTATCGCTTATGCAATGATCAACCAAGAAATCTCTAATGAATTAGTATTGATCGATGTG | 144 |
| Qy | 42 | ValProAsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValValAsp | 61 |
| Db | 145 | AATCAAGRAAAAGCAGAGGGGAACGATTCGACCTTTAGTAGTGGTTCGGCGCAT | 204 |
| Qy | 62 | ThrGlyIleThrValTyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspValVal | 81 |
| Db | 205 | GAATAATGGCGCTGTATGG---TCAGGTGGCTATGAAGAATGTAAGATGCTGATATCGTT | 261 |
| Qy | 82 | IleIleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArgMet | 101 |
| Db | 262 | GTTATCACAGCTGGTATCAACCAAAACCTGGTCAA-----TCTCGTTTA | 306 |
| Qy | 102 | AspLeuLeuProValAsnIleLysIleMetArgGluValValGlyAlaAlaIleLysSerTyr | 121 |
| Db | 307 | GATTAGTTAAACAANAATCGCTCAATCATCGCCCAATCGTAAAGAANAATCATGGGATCA | 366 |
| Qy | 122 | CysProAsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeu | 141 |
| Db | 367 | GGATTCGACGGTATTATCGTTGTGCTTCAAACCCAGTAGATATTTGCATATATATCGCT | 426 |
| Qy | 142 | GlnGluSerSerGlyLeuProHisIleArgIleCysGlyMetAlaGlyMetLeuAspSer | 161 |
| Db | 427 | TGGAACGAATCTGGTCTGCCAACATCATCGTGTATTATCGGTACTGGAACAAACATTGGATACA | 486 |
| Qy | 162 | SerArgPheArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGly | 181 |
| Db | 487 | ACTCGTTCCGTAAGAANAATCGCATTTGAAATTTAAAGTTGACCCACGACCGCTCCACGGC | 546 |
| Qy | 182 | MetValIleGlyValHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsn | 201 |
| Db | 547 | TATATCTTAGGTGAACATGGTCATTTCAGAGATCTCTCATGCTGGTTCACATCAACTCTCGGT | 606 |

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 23:54:34 ; Search time 3708 Seconds
(without alignments)
4163.899 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVFEKTRPKIANVGSGLI.....GSIDEVEMQKATAALDASK 330

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/abs/ABSSWEB.spool/US09390846/runat_02032006_104232_4868/app.query.fasta_1
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06p
-USER=US09390846 @CGN 1.1 8010 @runat_02032006_104232_4868 -ICPU=3
-NO MMAP -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_gses.*
11: gb_gses.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 769 | 45.6 | 811 | 7 CV643661 | CV643661 EST922414 |
| 2 | 762 | 45.1 | 804 | 7 CV637221 | CV637221 EST915974 |
| 3 | 742.5 | 44.0 | 784 | 6 CB025968 | CB025968 T9ESTzyd3 |
| 4 | 741 | 43.9 | 777 | 7 CV637428 | CV637428 EST916181 |
| 5 | 721.5 | 42.7 | 753 | 6 CB025472 | CB025472 T9ESTzyc7 |
| 6 | 718 | 42.5 | 900 | 8 CX022234 | CX022234 EST940553 |
| 7 | 702 | 41.6 | 684 | 7 CV551869 | CV551869 T9ESTzyq4 |

| | | | | | | |
|----|-------|------|-----|---|----------|--------------------|
| 8 | 686.5 | 40.7 | 772 | 6 | CB022051 | T9ESTzyc9 |
| 9 | 683.5 | 40.5 | 780 | 6 | CB030949 | CB030949 T9ESTzyd4 |
| 10 | 674.5 | 40.0 | 721 | 6 | CB027630 | CB027630 T9ESTzyc9 |
| 11 | 671.5 | 39.8 | 630 | 6 | CF259970 | CF259970 NCEST3c91 |
| 12 | 659 | 39.0 | 586 | 6 | CF268212 | CF268212 T9ESTzyj1 |
| 13 | 658 | 39.0 | 628 | 7 | CN621209 | CN621209 T9ESTzym8 |
| 14 | 656.5 | 38.9 | 744 | 6 | CB025686 | CB025686 T9ESTzyx8 |
| 15 | 656.5 | 38.9 | 746 | 7 | CK734706 | CK734706 T9ESTzyk7 |
| 16 | 653 | 38.7 | 585 | 6 | CB301250 | CB301250 T9ESTzyf5 |
| 17 | 651.5 | 38.6 | 766 | 6 | CB024558 | CB024558 T9ESTzyd0 |
| 18 | 650 | 38.5 | 611 | 6 | CB754431 | CB754431 T9ESTzyh9 |
| 19 | 645 | 38.2 | 595 | 6 | CF659673 | CF659673 NCEST3c51 |
| 20 | 641.5 | 38.0 | 752 | 6 | CB023734 | CB023734 T9ESTzyc5 |
| 21 | 636.5 | 37.7 | 577 | 6 | CF268385 | CF268385 T9ESTzyj2 |
| 22 | 623 | 36.9 | 602 | 6 | CF421715 | CF421715 NCEST3d84 |
| 23 | 621.5 | 36.8 | 714 | 7 | CK734359 | CK734359 T9ESTzyk7 |
| 24 | 620 | 36.7 | 691 | 6 | CB065846 | CB065846 PVBE05B11 |
| 25 | 619.5 | 36.7 | 580 | 6 | CF341663 | CF341663 T9ESTzyj3 |
| 26 | 618 | 36.6 | 746 | 8 | CX022116 | CX022116 EST940435 |
| 27 | 613.5 | 36.3 | 582 | 6 | CB411873 | CB411873 T9ESTzyh5 |
| 28 | 613.5 | 36.3 | 615 | 7 | CN122464 | CN122464 T9ESTzyf0 |
| 29 | 611.5 | 36.2 | 576 | 6 | CB301358 | CB301358 T9ESTzyf5 |
| 30 | 611 | 36.2 | 690 | 3 | BM169276 | BM169276 EST571799 |
| 31 | 608 | 36.0 | 577 | 7 | CF967655 | CF967655 NCESTqac1 |
| 32 | 607 | 36.0 | 571 | 7 | CO053115 | CO053115 T9ESTzyh8 |
| 33 | 605.5 | 35.9 | 709 | 7 | CV702488 | CV702488 T9ESTzyf7 |
| 34 | 601.5 | 35.6 | 580 | 6 | CF268206 | CF268206 T9ESTzyj1 |
| 35 | 601.5 | 35.6 | 582 | 7 | CF942651 | CF942651 NCESTqac0 |
| 36 | 598 | 35.4 | 770 | 1 | AJ821572 | AJ821572 T9ESTzyf5 |
| 37 | 590 | 35.0 | 559 | 6 | CB367907 | CB367907 T9ESTzyg3 |
| 38 | 588.5 | 34.9 | 561 | 3 | BM175091 | BM175091 T9ESTzyb1 |
| 39 | 587 | 34.8 | 556 | 6 | CF247444 | CF247444 T9ESTzyi6 |
| 40 | 573 | 33.9 | 817 | 7 | CV647412 | CV647412 EST926165 |
| 41 | 565.5 | 33.5 | 537 | 3 | BM271642 | BM271642 T9ESTzyb5 |
| 42 | 562.5 | 33.3 | 716 | 7 | CV549539 | CV549539 T9ESTzyr6 |
| 43 | 562 | 33.3 | 535 | 7 | CN196747 | CN196747 T9ESTzym0 |
| 44 | 560.5 | 33.2 | 526 | 6 | CB187397 | CB187397 T9ESTzyf4 |
| 45 | 558 | 33.1 | 576 | 7 | CN621319 | CN621319 T9ESTzym8 |

ALIGNMENTS

| RESULT 1 | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM | REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|----------|-----------|----------------------------|-----------|-------------|------------------|------------------|--|--------------------|---------------------------|---|--------------------|--|
| CV643661 | EST922414 | Field isolate cDNA library | CV643661 | EST | Plasmodium vivax | Plasmodium vivax | Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. | 1 (bases 1 to 811) | Carlton, J.M. and Cui, L. | A survey of genes in Plasmodium vivax by EST sequencing | Unpublished (2004) | Contact: Jane Carlton Parasite Genomics Group The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-530-9319 Fax: 301-838-0208 Email: carlton@tigr.org |
| CV643661 | PVMEZ82 | 5' end, mRNA sequence. | CV643661 | GI:56950479 | EST | Plasmodium vivax | Plasmodium vivax | 1 (bases 1 to 811) | Carlton, J.M. and Cui, L. | A survey of genes in Plasmodium vivax by EST sequencing | Unpublished (2004) | Contact: Jane Carlton Parasite Genomics Group The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-530-9319 Fax: 301-838-0208 Email: carlton@tigr.org |

| FEATURES | Location/Qualifiers |
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| | /mol_type="mRNA" |
| | /strain="Field isolate" |
| | /db_xref="taxon:5855" |
| | /clone_lib="Field isolate cDNA library" |


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Db      365  GTGATGTGTGCGAGTTACTCTTCGAGCATTTCCGGAGTCCCAAAAATAAATCATCGGATTA 424
Qy      156  AlaGlyMetLeuAspSerSerArgPheArgMetIleAlaAspLysLeuGluValSer 175
Db      425  GGTGGTGTGTAGATACATCTAGACTGAATATTTACATATCGCGAGAAGTTGAACTCCGC 484
Qy      176  ProArgAspValGlnGlyMetValIleGlyValHisGlyAspHisMetValProLeuSer 195
Db      485  CCGAGAGATGTTATGCACCTATGTCGTGCACATGGACACAGATGGTTCTCTCTGAAA 544
Qy      196  ArgTyrAlaThrValAlaGlnGlyProLeuSerGluPheValLysLysGlyTyrIleLys 215
Db      545  AGGTACATCACAGTTGAGGTATCCCATGTCGAAGATTTTATTAATAACAAAAGATTACA 604
Qy      216  GlnGluValAspAspIleValGlnLysThrLysValAlaGlyGlyGluIleValArg 235
Db      605  GATGAAGAAGTGAAGGACATATTTGATCGCACTGTGAACACTGCTTTTCGAGATTGTGAGC 664
Qy      236  LeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGlu 255
Db      665  CTCCTT-----GCCTCTCCTTATGTTGCCCACTGCTGCCATCATCGAAATGCCGAA 718
Qy      256  SerTyrLeuLysAspArgLysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyr 275
Db      719  TCTATTGGAAGGATATAGAAGAGTCTGTTGTTCCACTCTACTAGAGGACATAC 778
Qy      276  GlyValGlnAlaHisTyrLeuGly 283
Db      779  GGCCACAGCAACATCTTTGGTGGT 802

RESULT 3
CB025968
LOCUS
DEFINITION
  TgESTzyd32a10.y1 TGRH Tachyzoite Norm 7 cDNA Library Toxoplasma
  gondii cDNA clone TgESTzyd32a10.y1 5' similar to TR:P90613 P90613
  LACTATE DEHYDROGENASE ;, mRNA sequence.
ACCESSION
CB025968
VERSION
CB025968.1 GI:27722340
KEYWORDS
EST.
SOURCE
Toxoplasma gondii
ORGANISM
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
REFERENCE
1 (bases 1 to 784)
  Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajikwa,J.A., White,M.,
  Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
  Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
  Ritter,E., Bennett,J., Franklin,C., Tsagaris,I., Ronko,I.,
  Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
  Toxoplasma EST Project
  Unpublished (2001)
  Contact: Clifton, S.
  Toxoplasma EST project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: toxo@wustl.edu
  Contact David Sibley (toxost@borcim.wustl.edu) for further
  information relating to organism, libraries, or clone availability.
  Seq primer: -40RP from Gibco
  High quality sequence stop: 440.
  Location/Qualifiers
    source
      1..784
        /organism="Toxoplasma gondii"
        /mol_type="mRNA"
        /strain="RH (Type 1)"
        /db_xref="taxon:5811"

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/clone="TgESTzyd32a10.y1"
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/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="TGRH Tachyzoite Norm 7 cDNA Library"
/notes="Vector: pBluscript SK-; Site 1: EcoRI; Site 2:
XhoI; Toxoplasma RH strain tachyzoites were grown in human
foreskin fibroblast cultures in vitro. The library was
originally constructed by K.L.Wan, Cambridge University.
cDNAs were synthesized from polyA RNAs by oligo d(T)
priming and directionally cloned into the EcoRI to XhoI
sites of the Lambda ZapII vector using the ZAP-cDNA
synthesis kit (Stratagene). The primary cDNA library was
mass excised as phagemid using ExAssist helper phage
(Suratagene). Phagemid DNA was extracted by
phenol-chloroform method, and hybridized against a pool of
highly abundant genes which were derived from short-cycle
PCR of the primary cDNA library. The normalized library
was electroporated into DH10B (GeneHog, Invitrogen, Inc).
WARNING: the library contains a small percentage of cDNAs
derived from the human host cells."

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ORIGIN

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Alignment Scores:
Pred. No.:      2,47e-76      Length:      784
Score:          742.50      Matches:    140
Percent Similarity: 77.3%      Conservative: 34
Best Local Similarity: 62.2%      Mismatches: 50
Query Match:    44.0%      Indels:     1
DB:             6          Gaps:        1

US-09-390-846-2 (1-330) x CB025968 (1-784)
Qy      9   ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db      110 AGAAGAGAGGTGGCCATGATGGCTCTGGCATGTTGGTGCACTATGGCTACCTGCTGC 169
Qy      29   SerLeuArgGluLeuGlyAspValValLeuPheAspValValProMetMetGly 48
Db      170 GCTCTCCGTGAGTCGTCGTCGCTGCTTCTCTACGATGTTGTCAAGATGATGCCGAGGT 229
Qy      49   LysAlaMetAspIleSerHisAenSerSerValValAspThrGlyIleThrValTyrGly 68
Db      230 AAGGCTCTTGACCTGAGCCATGACCTCGCTGGTGACACCAACGTTCCCGTCGTGCT 289
Qy      69   SerAsnSerTyrGlu---CysLeuLysGlyValAlaAspValValIleIleThrAlaGlyIle 87
Db      290 GAGTACTCTTACGAGCGCGCTCACCGGTGGGAGTATGCTTATCGTACCGCGGTCTG 349
Qy      88   ThrLysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsn 107
Db      350 ACCAAGTGTGGGGCAAGCCGAGCTCCGAGTGGAGCGCAACGATCTGCTCCGCTTCAAC 409
Qy      108 IleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheVal 127
Db      410 TCGAAGATCATTCGCGAGATCGGTGAGACATCAAGAAGTACTGCCCAAGACCTTCATC 469
Qy      128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeu 147
Db      470 ATGCTGGTACCACACCGCTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
Qy      148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
Db      530 CCGACCAACATGATCTCGGTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
Qy      168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
Db      590 GTCCGCGAGCGGCTCTCTGCTCTCCCGCGAGCTCCAGGCCACCGCTCATCGCACAC 649
Qy      188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu 207
Db      650 GGCCTTGTGATGTCCTCGCTTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
Qy      208 PheValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLys 227

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| | | | |
|---|-----|---|-----|
| QY | 146 | GlyLeuProHisHisArgGlyCysGlyMetAlaGlyMetLeuAspSerArgPheArg | 165 |
| DB | 271 | GGAGTCCCAAAATAAATATCATCGATTAGGTGGTGTAGATACATCTAGACTGAAA | 330 |
| QY | 166 | ArgMetIleAlaAspTysLeuGluValSerProArgAspValGlnGlyMetValIleGly | 185 |
| DB | 331 | TATTACATATCGCAGAAAGTTGAAGCTGTGCCGAGAGATGTTAATGCACCTCAITGTGGT | 390 |
| QY | 186 | ValHisGlyAspHisMetValProLeuSerArgTyrAlaThrValIleGlyProLeu | 205 |
| DB | 391 | GCACATGGGAACAAGATGGTTCTCTGAAAAGGTACATCACAGTTGGAGGTATCCCATTTG | 450 |
| QY | 206 | SerGluPheValIleGlyTyrPheValGlnGlyValAspIleValGlnLys | 225 |
| DB | 451 | CAAGAATTTATTAACAAGAAATACAGATGAAGAGTGAAGGCATATTTGTATCGC | 510 |
| QY | 226 | ThrLysValAlaGlyGlyIleValArgLeuGlyGlnGlySerAlaTyrTyrAla | 245 |
| DB | 511 | ACTGTGAACACTGCTTTGGAGATTGTGAACCTCCTT-----GCCCTCCTTATGTGCC | 564 |
| QY | 246 | ProGlyAlaSerAlaIleGlnMetAlaGluSerTyrIleLysAspArgLysArgValMet | 265 |
| DB | 565 | CCAGCTGCTCCCATCATCGAAATGGCCGAATCTTATTGTAAGGATATAAAGAAAGTGCTT | 624 |
| QY | 266 | ValCysSerCysTyrLeuGlnGlyTyrGlyValGlnAenHisTyrLeuGlyValPro | 285 |
| DB | 625 | GTGTGTTCCACTTACTAGAGGACATACAGCCACAGCAACATCTTTGGTGGTACTCCT | 684 |
| QY | 286 | CysValIleGlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGlu | 305 |
| DB | 685 | CTCGTTATCGGGGCACCGGAGTTGAGCAAGTCATCGAGTTGCAGCTGTAATGCCGAGGAG | 744 |
| QY | 306 | ArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIle | 323 |
| DB | 745 | AAGACCAAGTTTCGACGAGGCGAGTTGCGGAGACTAAAGGATGAAGGCGCTCATT | 798 |
| RESULT 7 | | | |
| CV551869 | | | |
| LOCUS | | | |
| DEFINITION | | | |
| TgESTzyq47c09.y3 Ty COUG Tachyzoite cDNA library Toxoplasma gondii | | | |
| cDNA clone TgESTzyq47c09.y3 5' similar to TR:P90613 P90613 LACTATE | | | |
| DEHYDROGENASE ; mRNA sequence. | | | |
| CV551869 | | | |
| CV551869.1 GI:54431926 | | | |
| EST. | | | |
| Toxoplasma gondii | | | |
| Toxoplasma gondii | | | |
| Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; | | | |
| Sarcocystidae; Toxoplasma. | | | |
| 1 (bases 1 to 684) | | | |
| Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M., | | | |
| Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., | | | |
| Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., | | | |
| Ritter,E., Bennett,J., Franklin,C., Teagareishvili,R., Ronko,I., | | | |
| Kennedy,S., Maguire,L., Waterston,R. and Wilson,R. | | | |
| Toxoplasma EST Project | | | |
| Unpublished (2001) | | | |
| Contact: Clifton, S. | | | |
| Toxoplasma EST Project | | | |
| Washington University School of Medicine | | | |
| 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA | | | |
| Tel: 314 286 1800 | | | |
| Fax: 314 286 1810 | | | |
| Email: toxowatson.wustl.edu | | | |
| Contact David Sibley (toxoes@borcim.wustl.edu) for further | | | |
| information relating to organism, libraries, or clone availability. | | | |
| Seq primer: T7 from Gibco | | | |
| High quality sequence stop: 584. | | | |
| Location/Qualifiers | | | |
| 1..684 | | | |
| /organism="Toxoplasma gondii" | | | |
| /mol_type="mRNA" | | | |
| FEATURES | | | |
| source | | | |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. No.: 1.18e-71 Length: 684 | | | |
| Score: 702.00 Matches: 128 | | | |
| Percent Similarity: 74.6% Conservative: 42 | | | |
| Best Local Similarity: 56.1% Mismatches: 58 | | | |
| Query Match: 41.6% Indels: 0 | | | |
| DB: 7 Gaps: 0 | | | |
| US-09-390-846-2 (1-330) x CV551869 (1-684) | | | |
| QY | 83 | IleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAsp | 102 |
| DB | 1 | GTATCCGCGGTCTGACCAAGGTGCGGCAAGCCGACTCCGAGTGGAGCCGAAACGAT | 60 |
| QY | 103 | LeuLeuProValAsnIleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCys | 122 |
| DB | 61 | CTGCTCCCTTCAACTCGAAGATCATTCGCGAGATCGGTGAGAACATCAAGAGTACTGC | 120 |
| QY | 123 | ProAsnAlaPheValIleAenIleThrAenProLeuAspValMetValAlaLeuGln | 142 |
| DB | 121 | CCCAAGACCTTATCATCTGCTGTCACCAACCCGCTGGACTGTCATGTCAGGTCAATGTC | 180 |
| QY | 143 | GluSerSerGlyLeuProHisArgIleCysGlyMetAlaGlyMetLeuAspSerSer | 162 |
| DB | 181 | GAGGCTCTGGCGTCCCGACCAACATGATCTGCGGTATGCGCTGTCATGTCGACTCTGGT | 240 |
| QY | 163 | ArgPheArgMetIleAlaAspLysLeuGluValSerProArgAspValGlnGlyMet | 182 |
| DB | 241 | CGCTCCGCGGATACGTCCCGACGCGCTGTCGTCTCTCCCGCGACGTCACGCGCAC | 300 |
| QY | 183 | ValIleGlyValHisGlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGly | 202 |
| DB | 301 | GTATCCGCGCACACGCGGACTGCATGTTGTCGCTTGTCCGGTACATTACCGTGAACGCG | 360 |
| QY | 203 | IleProLeuSerGluPheValLysGlyTyrPheLysGlnGluValAspAspIle | 222 |
| DB | 361 | TACCCGATCCATAAGTTTCATCGAGGACGCGTAGTCACGGAAGCATCTCGAGGAGATC | 420 |
| QY | 223 | ValGlnLysThrLysValAlaGlyGlyIleValArgLeuLysGlnGlySerAla | 242 |
| DB | 421 | GCTGACACACCAAAAGTGTCTGCGCGGAGATCGTCCGCTTCTCCGCGGGGTCTCTCT | 480 |
| QY | 243 | TyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLys | 262 |
| DB | 481 | TACTAGCCCCCGCGCATCCGCTGCGGCATGGCAACATCTTCTTGAACGACAAAG | 540 |
| QY | 263 | ArgValMetValCysSerCysTyrLeuGlnGlyTyrGlyValGlnAenHisTyrLeu | 282 |
| DB | 541 | CGCGTTCATCCGTGAGTGTGTAACGAGGAGTACGGCTTAGAGGACATGTGCTTT | 600 |
| QY | 283 | GlyValProCysValIleGlyGlyArgGlyValGluLysIleIleGluLeuGluThr | 302 |
| DB | 601 | TGCTCTCCCGCGGTCAATGGAGGCGCTGGCATCGACCCGCGTCATCGAGCTCAAGCTGAAC | 660 |
| QY | 303 | AlaGlnGluArgGlnGluLeuGln | 310 |

/db_xref="taxon:5811"
 /clone="TgESTzyq47c09.y3"
 /dev_stage="Tachyzoite"
 /lab_host="GC10 Competent Cells (PGC)"
 /clone_lib="Ty COUG Tachyzoite cDNA Library"
 /note="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; The
 cDNA library was constructed by Keliang Tang, and Robert
 Cole at Washington University. Total RNA was converted to
 cDNA using the template-switching PCR method (Creator
 SMART cDNA, Clontech Inc.). First strand was PCR amplified
 using the same primer set and the fragments were digested
 with SfiI. The fragments were size selected, ligated into
 vector pDNR LIB containing directional SfiI sites, and
 electroporated into GC10 competent cells. WARNING: the
 library contains a small percentage of cDNAs derived from
 the human host cells."

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco
High quality sequence stop: 436.

FEATURES

source

Location/Qualifiers

1..780
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/strain="RH (Type I)"
/db_xref="taxon:5811"
/dev_stage="Tachyzoite"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="TGRH Tachyzoite Norm 7 cDNA Library"
/notes="Vector: pBluscript SK-; Site 1: EcoRI; Site 2: XhoI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L.Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the Lambda ZapII vector using the ZAP-cDNA synthesis kit (Stratagene). The primary cDNA library was mass excised as phagemid using ExAssist helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short-cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (GeneHog, Invitrogen, Inc). WARNING: the library contains a small percentage of cDNAs derived from the human host cells."

ORIGIN

Alignment Scores:
Pred. No.: 2,17e-69 Length: 780
Score: 683.50 Matches: 131
Percent Similarity: 77.1% Conservative: 24
Best Local Similarity: 65.2% Mismatches: 45
Query Match: 40.5% Indels: 1
DB: 6 Gaps: 1

US-09-390-846-2 (1-330) x CB030949 (1-780)

QY 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
DB 177 AGAAGAGGTGCCATGATGGCTTGGCATGATTGGTGGCACTATGGCTACCTGTGC 236
QY 29 SerLeuArgGluLeuGlyAspValValPheAspValValProAsnMetProMetGly 48
DB 237 GCTCTCCGTGAGCTCGCTGACGTCGTCTCTACGATGTTGTCAAAGGTATGCCGAGGCT 296
QY 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
DB 297 AAGGCTCTTGACCTGAGCCATGACCTCGGTGGTGCACACCAACATGCTCCGTCGTGT 356
QY 69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleIleThrAlaGlyIle 87
DB 357 GAGTACTCTTACAGGCGCGCTCACCGGTGGCATGTGGTTATCGTTACCGCGGCTGTG 416
QY 88 ThrLysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsn 107
DB 417 ACCAAGGTGCCGGCAAGCCGACTCCGAGTGGAGCCGAACATGCTGCTCCGTTCAAC 476
QY 108 IleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheVal 127
DB 477 TCGAAGATCATTCGCGAGATCGCTCAGAACATCAAGAAGTACTGCCCAAGACCTTCATC 536
QY 128 IleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGlnSerSerGlyLeu 147
DB 537 ATCGTGGTCACCAACCGCTGGACTGCATGGTCAAGTTATGTGCCGAGGCTCTGCGCTC 596
QY 148 ProHisHieArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
DB 597 CCGACCAACATGATCTGCGGTATGGCTGCATGCTCGACTCTGTGCTTCGCGCCGATAC 656

QY 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
DB 657 GTCCGCGAGCGCTCTCTGTCTCTCCCGGACGTCACAGGCCACCGTATCCGCACAC 716
QY 188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu 207
DB 717 GCGGACTGCATGGTCCCGCTTGTCCGGTACATTACCGTGAACGGCTACCCGATCCAGAAG 776
QY 208 Phe 208
DB 777 TTC 779

RESULT 10

CB027630

LOCUS

DEFINITION

CB027630 721 bp mRNA linear EST 13-JAN-2003
TgESTzyc98c08.y1 TGRH Tachyzoite Norm 5 cDNA Library toxoplasma
gondii cDNA clone TgESTzyc98c08.y1 5' similar to TR:P90613 P90613
LACTATE DEHYDROGENASE ; mRNA sequence.

ACCESSION

CB027630

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..721

/organism="Toxoplasma gondii"

/mol_type="mRNA"

/strain="RH (Type I)"

/db_xref="taxon:5811"

/clone="TgESTzyc98c08.y1"

/dev_stage="Tachyzoite"

/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"

/clone_lib="TGRH Tachyzoite Norm 5 cDNA Library"

/note="Vector: pBluscript SK-; Site 1: EcoRI; Site 2: XhoI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L.Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the Lambda ZapII vector using the ZAP-cDNA synthesis kit (Stratagene). The primary cDNA library was mass excised as phagemid using ExAssist helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short-cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (GeneHog, Invitrogen, Inc). WARNING: the library contains a small percentage of cDNAs derived from the human host cells."

ORIGIN

Alignment Scores:

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco
High quality sequence stop: 567.

FEATURES

source

1. 628
/organism="Toxoplasma gondii"

/mol_type="mRNA"

/strain="tachyzoite"

/db_xref="taxon:5811"

/clones="TgESTzym82h11.y1"

/dev_stage="tachyzoite"

/lab_host="ElectroTen Blue cells (Stratagene)"

/clone_lib="TgMAS Tachyzoite cDNA Library"

/note="vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed by Kellang Tang, and Robert Cole at Washington University. cDNA was synthesized from Poly(A)+ mRNA using an oligo-d(T) primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA, and products were size-selected on Sephadryl S500. The cDNA were directionally cloned into the EcoRI/XhoI prepared pBluescript II SK+ vector, and electroporated into ElectroTen Blue cells (Stratagene). The library may contain a small percentage of host or bacterial contaminants."

ORIGIN

Alignment Scores:
Pred. No.: 1.57e-66 Length: 628
Score: 658.00 Matches: 122
Percent Similarity: 75.8% Conservations: 35
Best Local Similarity: 58.9% Mismatches: 50
Query Match: 39.0% Indels: 0
DB: 7 Gaps: 0

US-09-390-846-2 (1-330) x CN621209 (1-628)

Qy 95 AspLysGluTrpSerArgMetAspLeuLeuProValAsnLeuLeuMetArgGluVal 114
Db 2 GACTCCGAGTGGAGCCGACCATCTGCTCCGTTCAACTCGAAGATCATTCGCGATC 61
Qy 115 GlyAlaAlaLeuSerTyrCysProAsnAlaPheValLeuLeuAsnLeuLeuProLeu 134
Db 62 GGTGAGAACATCAAGAGTACTGCCCCAAGACCTTCATCATCGGTGTCACCAACCCGCTG 121
Qy 135 AspValMetValAlaLeuGlnGluSerSerGlyLeuProHisHisArgLeuCysGly 154
Db 122 GACTGATGTCAAGTTATGTGCGAGGCTCTGGCGTCCGACCATCATGATCTCGGT 181
Qy 155 MetAlaGlyMetLeuAspSerSerArgPheArgMetLeuAlaAspLysLeuGluVal 174
Db 182 ATGGCTGTGATCTCGACTCTGTGCTGCTCCGCGATACGTCCGCGACGCGCTCTCTGTC 241
Qy 175 SerProArgAspValGlnGlyMetValLeuGlnHisGlyAspHisMetValProLeu 194
Db 242 TCTCCCGCGAGCTCCAGGCCACCGTTCATCGGCACACACGCGGACTCATGGTCCGCTT 301
Qy 195 SerArgTyrAlaThrValAsnGlyLeuProLeuSerGluPheValLysGlyTrpIle 214
Db 302 GTCCGGTACATTACCGTGAACGGTACCCGATCAGAAAGTTTCATCAGGACGGGTAGTC 361
Qy 215 LysGlnGluValAspAspIleValGlnLysThrLysValAlaGlyGlyGluLeuVal 234
Db 362 ACGGAGAAGCAGCTCGAGGAGATCGCTGAGCACACCAAAAGTGTCTGCGCGGAGATCGTC 421
Qy 235 ArgLeuLeuGlnGlySerAlaTyrTyrAlaProGlyAlaSerAlaLeuMetAla 254
Db 422 CGCTTCCTCGCGAGGTTTCGCTTACTAGCCGCCCGCCGATCCGCTGTGCGCATGGCA 481
Qy 255 GluSerTyrLeuLysAspArgLysArgValMetValCysSerCysTyrLeuGlnGlyGln 274
Db 482 ACATCTCTTGAACGACGAAAGCGCGTTCATCCCGTGCAGTGTGTACTGCAACGGAGAG 541

Qy 275 TyrGlyValGlnAsnHisTyrLeuGlyValProCysValLeuGlyArgGlyValGlu 294
Db 542 TAGCGGTTGAAGGACATGTTTCATTGGTCCCGCGGCGTTCATTGGAGCGCCCGCACCAG 601
Qy 295 LysIleLeuGluLeuGluLeu 301
Db 602 CGGTCATCCAGTCCAGCTG 622
RESULT 14
LOCUS CB025686
DEFINITION
TgESTzyc83a05.y1 TgrH Tachyzoite Norm 5 cDNA Library Toxoplasma gondii cDNA clone TgESTzyc83a05.y1 5' similar to TR:P90613 P90613 LACTATE DEHYDROGENASE ; mRNA sequence.
ACCESSION CB025686
VERSION 1 GI:27702659
KEYWORDS
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
REFERENCE 1 (bases 1 to 744)
AUTHORS Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
TITLE Toxoplasma EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxoe@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 434.
FEATURES
source
1. 744
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/strain="RH (Type I)"
/db_xref="taxon:5811"
/clone="TgESTzyc83a05.y1"
/dev_stage="tachyzoite"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="TgrH Tachyzoite Norm 5 cDNA Library"
/notes="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was originally constructed by K.L.Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the Lambda ZapII vector using the ZAP-cDNA synthesis kit (Stratagene). The primary cDNA library was mass excised as phagemid using EXassist helper phage (Stratagene). Phagemid DNA was extracted by phenol-chloroform method, and hybridized against a pool of highly abundant genes which were derived from short-cycle PCR of the primary cDNA library. The normalized library was electroporated into DH10B (GeneHog, Invitrogen, Inc). WARNING: the library contains a small percentage of cDNAs derived from the human host cells."

ORIGIN

Alignment Scores:

Pred. No.: 3.05e-66 Length: 744
Score: 656.50 Matches: 127
Percent Similarity: 77.2% Conservations: 22
Best Local Similarity: 65.8% Mismatches: 43

Query Match: 38.9% Indels: 1
 DB: 6 Gaps: 1

US-09-390-846-2 (1-330) x CB025686 (1-744)

QY 9 ArgProlyleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
 DB 166 AGAAGAAGTGGCCATGATTGGCTCTGGCATGATTGGTGGCACTATGGCTACCTGTGC 225

QY 29 SerLeuArgGluLeuGlyAspValValPheAspValValProAsnMetProMetGly 48
 DB 226 GCTCTCGGTGAGTCTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285

QY 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
 DB 286 AAGCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 345

QY 69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleThrAlaGlyIle 87
 DB 346 GAGTACTCTTACGAGGCGCGCTCACCGGTGGGACTGCGTTATCGTTACCGCGGTCTG 405

QY 88 ThrIysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsn 107
 DB 406 ACCAAGGTGGCGGCAAGCCGACTCCGAGTGGAGCGAAGCATCTGCTCCGTTCAAC 465

QY 108 IleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheVal 127
 DB 466 TCGAAGATCATCTCCGAGATCGGTGAGAACATCAAGACTGCCCCAAGACCTTCATC 525

QY 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlySerGlyLeu 147
 DB 526 ATCGTGTGACCAACCGCTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585

QY 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
 DB 586 CCGACCAACATGATCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645

QY 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
 DB 646 GTCGCCGACCGCTCTCTGCTCTCTCCCGCGAGCTCCAGGCCCGCTCATCGGCACAC 705

QY 188 GlyAspHisMetValProLeuSerArgTyrAlaThrVal 200
 DB 706 GCGGACTGCATGTGCTCCGCTTGTCCGCTACATACCGTG 744

RESULT 15
 CK734706
 LOCUS
 DEFINITION
 746 bp mRNA linear EST 17-FEB-2004
 TgESTzyk78e12.y1 TGRH Tachyzoite FL cDNA Toxoplasma gondii cDNA
 clone TgESTzyk78e12.y1 5' similar to TR:P90613 P90613 LACTATE
 DEHYDROGENASE ; mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Toxoplasma gondii
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Toxoplasma.
 1 (bases 1 to 746)

REFERENCE
 AUTHORS
 Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagaris,I., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilsson,R.
 Toxoplasma EST Project
 Unpublished (2001)
 CONTACT: Clifton, S.
 Toxoplasma EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: toxo@watson.wustl.edu

FEATURES
 source
 Location/Qualifiers
 1..746
 /organism="Toxoplasma gondii"
 /mol_type="mRNA"
 /db_xref="taxon:5811"
 /clone="TgESTzyk78e12.y1"
 /dev_stage="Tachyzoite"
 /lab_host="QC10"
 /clone_lib="TGRH Tachyzoite FL cDNA"
 /note="Vector: pDNR-Lib; Site 1: SfiI; Site 2: SfiI; The cDNA library was constructed by Kelian Tang, adn Robert Cole at Washington University. Total RNA was converted to cDNA using the template-switching PCR method (Creator SMART cDNA, Clontech, Inc.). First strand was reverse transcribed using the CDS III/3' primer and a 5' template switch primer using the same primer set and the fragments were digested with SfiI. The directional SfiI sites, and electroporated into GC10 Competent cells. Antibiotic: Chloramphenicol (30ug/ml)"

ORIGIN
 Alignment Scores:
 Pred. No.: 3,06e-66 Length: 746
 Score: 656.50 Matches: 127
 Percent Similarity: 77.2% Conservative: 22
 Best Local Similarity: 65.8% Mismatches: 43
 Query Match: 38.9% Indels: 1
 DB: 7 Gaps: 1

US-09-390-846-2 (1-330) x CK734706 (1-746)

QY 9 ArgProlyleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
 DB 168 AGAAGAAGTGGCCATGATTGGCTCTGGCATGATTGGTGGCACTATGGCTACCTGTGC 227

QY 29 SerLeuArgGluLeuGlyAspValValPheAspValValProAsnMetProMetGly 48
 DB 228 GCTCTCGGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287

QY 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
 DB 288 AAGCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 347

QY 69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleThrAlaGlyIle 87
 DB 348 GAGTACTCTTACGAGGCGCGCTCACCGGTGGGACTGCGTTATCGTTACCGCGGTCTG 407

QY 88 ThrLysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsn 107
 DB 408 ACCAAGGTGGCGGCAAGCCGACTCCGAGTGGAGCGAAGCATCTGCTCCGTTCAAC 467

QY 108 IleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheVal 127
 DB 468 TCGAAGATCATCTCCGAGATCGGTGAGAACATCAAGACTGCCCCAAGACCTTCATC 527

QY 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGlySerGlyLeu 147
 DB 528 ATCGTGTGACCAACCGCTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587

QY 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
 DB 588 CCGACCAACATGATCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647

QY 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
 DB 648 GTCGCCGACCGCTCTCTGCTCTCTCCCGCGAGCTCCAGGCCCGCTCATCGGCACAC 707

QY 188 GlyAspHisMetValProLeuSerArgTyrAlaThrVal 200
 DB 706 GCGGACTGCATGTGCTCCGCTTGTCCGCTACATACCGTG 744

Db 708 GCGACTGCATGGTCCCGCTTGTCGGTACATTACCGTG 746

Search completed: March 3, 2006, 01:04:29
Job time : 3716 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 23:42:12 ; Search time 1114 Seconds

(without alignments)

1974.281 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVPEKTRPKIAMVGSGL.....GSIDEVKEMQKAIADASK 330

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delpop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB.spool/US09390846/runat_02032006_104229_4815/app_query.fasta.1
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US09390846 -CGEN 1.1 727 @runat_02032006_104229_4815 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21:*

1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
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9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|------------|--------------------|
| 1 | 1685 | 99.8 | 1679 | 2 AAT51370 | Eimeria 1 |
| 2 | 1034.5 | 61.3 | 1785 | 2 AAX91434 | Aax91434 T. gondii |
| 3 | 1034.5 | 61.3 | 1785 | 2 AAX91435 | Aax91435 T. gondii |
| 4 | 1034.5 | 61.3 | 1785 | 4 AAS42758 | Aas42758 T. gondii |

| | 5 | 1034.5 | 61.3 | 1785 | 4 | AAS42757 |
|----|--------|--------|------|------|-----------|---------------------|
| 6 | 1034.5 | 61.3 | 1785 | 10 | ADG17361 | Adg17361 T. gondii |
| 7 | 1034.5 | 61.3 | 1785 | 10 | ADG17363 | Adg17363 T. gondii |
| 8 | 880.5 | 52.2 | 960 | 13 | ADT43087 | Adt43087 Bacterial |
| 9 | 873.5 | 51.7 | 957 | 13 | ADS59454 | Ads59454 Bacterial |
| 10 | 873.5 | 51.7 | 960 | 13 | ADS62502 | Ads62502 Bacterial |
| 11 | 873.5 | 51.7 | 960 | 13 | ADS62887 | Ads62887 Bacterial |
| 12 | 862.5 | 51.1 | 933 | 13 | ADT45997 | Adt45997 Bacterial |
| 13 | 862 | 51.1 | 969 | 13 | ADS60073 | Ads60073 Bacterial |
| 14 | 850.5 | 50.4 | 963 | 13 | ADT42328 | Adt42328 Bacterial |
| 15 | 848.5 | 50.3 | 960 | 13 | ADS656026 | Ads656026 Bacterial |
| 16 | 847.5 | 50.2 | 960 | 13 | ADS58536 | Ads58536 Bacterial |
| 17 | 831.5 | 49.3 | 951 | 2 | AAQ72947 | Aaq72947 P. falcip |
| 18 | 831.5 | 49.3 | 951 | 2 | AAQ26909 | Aax26909 cDNA enco |
| 19 | 740 | 43.8 | 939 | 13 | ADT48486 | Adt48486 Bacterial |
| 20 | 709 | 42.0 | 945 | 13 | ADT42644 | Adt42644 Bacterial |
| 21 | 706 | 41.8 | 1912 | 2 | AAT17715 | Aat17715 Heat resi |
| 22 | 697 | 41.3 | 936 | 13 | ADT41767 | Adt41767 Bacterial |
| 23 | 694 | 41.1 | 870 | 14 | ACL69781 | ACL69781 M. xanthu |
| 24 | 694 | 41.1 | 1634 | 14 | ACL63878 | Adt44376 Bacterial |
| 25 | 689 | 40.8 | 855 | 13 | ADG61598 | Adg61598 Bacterial |
| 26 | 675.5 | 40.0 | 959 | 13 | ADG61598 | Adg61598 Bacterial |
| 27 | 672 | 39.8 | 927 | 13 | ADS57058 | Ads57058 Bacterial |
| 28 | 652.5 | 38.7 | 912 | 13 | ADS58414 | Ads58414 Bacterial |
| 29 | 649.5 | 38.5 | 978 | 13 | ADT43469 | Adt43469 Bacterial |
| 30 | 641 | 38.0 | 978 | 6 | ABN93233 | ABN93233 Staphyloc |
| 31 | 641 | 38.0 | 978 | 13 | ADS04190 | Ads04190 Staphyloc |
| 32 | 635 | 37.6 | 912 | 13 | ADS59185 | Ads59185 Bacterial |
| 33 | 635 | 37.6 | 951 | 13 | ADT45039 | Adt45039 Bacterial |
| 34 | 634 | 37.6 | 975 | 13 | ADS48079 | Ads48079 Bacterial |
| 35 | 632 | 37.4 | 5024 | 2 | AAQ55139 | Aaq55139 Staphyloc |
| 36 | 632 | 37.4 | 5024 | 8 | ABZ77355 | Abz77355 Nucleotid |
| 37 | 632 | 37.4 | 5024 | 10 | AAL51843 | Aal51843 Staphyloc |
| 38 | 628 | 37.2 | 897 | 13 | ADS57777 | Ads57777 Bacterial |
| 39 | 626.5 | 37.1 | 915 | 13 | ADS58980 | Ads58980 Bacterial |
| 40 | 625.5 | 37.1 | 927 | 13 | ADT44107 | Adt44107 Bacterial |
| 41 | 621 | 36.8 | 822 | 6 | ABK72765 | Abk72765 Bacillus |
| 42 | 605.5 | 35.9 | 1008 | 13 | ADS45395 | Ads45395 Bacterial |
| 43 | 569 | 33.7 | 1005 | 13 | ADS45382 | Ads45382 Bacterial |
| 44 | 560.5 | 33.2 | 942 | 13 | ADT48105 | Adt48105 Bacterial |
| 45 | 518 | 30.7 | 595 | 13 | ADS62339 | Ads62339 Bacterial |

ALIGNMENTS

RESULT 1
AAT51370
ID AAT51370 standard; cDNA to mRNA; 1679 BP.
XX
AC AAT51370;
XX
17-OCT-2003 (revised)
DT 29-APR-1997 (first entry)
XX
DE Eimeria lactate dehydrogenase cDNA clone EASC2.
XX
Lactate dehydrogenase; LDH; coccidiosis; vaccine; vector; ds.
XX
OS Eimeria acervulina; strain Houghton.
XX
Key Location/Qualifiers
FT misc_RNA 1..61
FT misc_RNA /tag= b
FT /note= "pBluescriptII derived sequence"
FT CDS 280..1272
FT /tag= a
FT /product= "lactate dehydrogenase"
FT misc_RNA 1624..1679
FT /tag= c
FT /note= "pBluescriptII derived sequence"
XX
PN AU9656287-A.
XX

PD 16-JAN-1997.
 XX
 PF 02-JUL-1996; 96AU-00056287.
 XX
 PR 03-JUL-1995; 95EP-00201801.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Kok JJ, Van Den Boogaart P, Vermeulen AN;
 XX WPI; 1997-109375/11.
 DR P-PSDB; AAW11476.
 XX
 XX Eimeria lactate dehydrogenase protein - used for prodn. of vaccines
 PT against coccidiosis in poultry.
 XX
 PS Claim 6; Page 20-22; 30pp; English.
 XX
 CC A cDNA clone (AAT51370), designated EASC2, codes for the 37 kDa lactate
 CC dehydrogenase (LDH) (AAW11476) of Eimeria acervulina schizonts. It was
 CC isolated from an E. acervulina oocyst cDNA library in phage lambda ZAPII
 CC by screening with antibodies raised against isolated LDH protein fraction
 CC EASC2. Nucleic acids encoding LDH, or immunologically active portions of
 CC it, can be used to produce LDH in host cells or organisms. The
 CC recombinant LDH, host organisms, recombinant viral vectors or naked LDH
 CC DNA can be utilised in vaccines for the protection of poultry against
 CC coccidiosis. (Updated on 17-Oct-2003 to standardise OS field)
 XX
 SQ Sequence 1679 BP; 449 A; 353 C; 408 G; 469 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5,99e-172 Length: 1679
 Score: 1685.00 Matches: 329
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 99.7% Mismatches: 0
 Query Match: 99.8% Indels: 0
 DB: 2 Gaps: 0

US-09-390-846-2 (1-330) x AAT51370 (1-1679)

Qy 1 MetAlaValPheGluLysAsnThrArgProLysIleAlaMetValGlySerGlyMetIle 20
 |||||
 Db 280 ATGCGGCTCTTCGAGAGATACACGCCCAAGATTGCTATGTTGGGCTCGGTATGATT 339
 |||||
 Qy 21 GlyGlyThrMetAlaPheLeuGlySerLeuArgGluLeuGlyAspValValLeuPheAsp 40
 |||||
 Db 340 GGAGGCCACCATGGCTTTCTGTCAGCTTGAGGAACTCGAGAGATGTTGCTCTTCGAC 399
 |||||
 Qy 41 ValValProAsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValVal 60
 |||||
 Db 400 GTTGATCCGAACATGCCGATGGGAAGCGGATGATATATCGCAAAATTGCTCGGTGGTT 459
 |||||
 Qy 61 AspThrGlyIleThrValTyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspVal 80
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 Db 460 GACACGGGTATACAGTATACGGCTCAAAATTCATACAGTCTTGAAGGGTGGCGACGTA 519
 |||||
 Qy 81 ValIleIleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArg 100
 |||||
 Db 520 GTAATAATAACAGCAGGAGTAACAAAGATATACCCGGAAGAGCGGATAAAGAATGCTTAGA 579
 |||||
 Qy 101 MetAspLeuLeuProValAsnIleValIleMetArgGluValGlyAlaAlaIleLysSer 120
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 Db 580 ATGGATCTATTACCTGTGAATATAAGATAATAGGAGCGCTCGGTGCGCAATTTAAATCT 639
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 Qy 121 TyrCysProAsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAla 140
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 Db 640 TACTGTCTTAATGATTTGTTATTATAATAACAATCTTTAGATGTGATGTTAGTCTGCT 699
 |||||
 Qy 141 LeuGlnGluSerSerGlyLeuProHisArgIleCysGlyMetAlaGlyMetLeuAsp 160
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 Db 700 CTTCAAGAGTTCATCAGGACTACCTCATCATAGATCTGCGGTATGCGTGGGATGCTTGTAT 759
 |||||
 Qy 161 SerSerArgPheArgMetIleAlaAspLysLeuGluValSerProArgAspValGln 180
 |||||

Db 760 AGCTCTCGTTTTAGACGTATGATAGCTATAAATTAGAAGTCTCTCTAGAGATGTACAG 819
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 Qy 181 GlyMetValIleGlyValHisGlyAspHisMetValProLeuSerArgTyrAlaThrVal 200
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 Db 820 GGGATGTCATAGGTGTACACGCGCATATATGGTCCCTTAAGTAGATATGCAACAGTT 879
 |||||
 Qy 201 AsnGlyIleProLeuSerGluPheValLysGlyTyrIleLysGlnGluGluValAsp 220
 |||||
 Db 880 AACGGCATCCCGCTTTCTGAGTTTGTAAAGAGGCTGGATCAAGCAAGAGAGTAGAT 939
 |||||
 Qy 221 AspIleValGlnLysThrLysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGly 240
 |||||
 Db 940 GATATCGTTTCAGAGACCAAGGTCGCTCGAGGAGAGATCGTACGCTATTAGCAAGGC 999
 |||||
 Qy 241 SerAlaTyrTyrAlaProGlyAlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAsp 260
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 Db 1000 TCTGCTTACTGCTCCAGGGCTTCAGCTATTTCAGATGCTGAGAGCTATCTTAAAGGAT 1059
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 Qy 261 ArgLysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHis 280
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 Db 1060 AGAAAGAGAGTGTATGTTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1119
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 Qy 281 TyrLeuGlyValProCysValIleGlyGlyArgGlyValGlyLysIleIleGluLeuGlu 300
 |||||
 Db 1120 TACTTAGGAGTACCTTGTGTATCGCTGGGAGAGGTTTGAGAAGATTATTGAGTTAGAA 1179
 |||||
 Qy 301 LeuThrAlaGlnGluArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGln 320
 |||||
 Db 1180 TTGACCCGACAAAGAACAGAGGAGCTTCAGGGATCTATCGATGAGGTTAAGGAGATGCAG 1239
 |||||
 Qy 321 LysAlaIleAlaAlaLeuAspAlaSerLys 330
 |||||
 Db 1240 AAGGCTTGTGCTCTTGTATGATCATCAAG 1269
 |||||

RESULT 2
 AAX91434
 ID AAX91434 standard; DNA; 1785 BP.
 XX AAX91434;
 AC AAX91434;
 DT 24-SBP-1999 (first entry)
 XX
 DE T. gondii MGIS6-5 DNA sequence.
 XX
 XX Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
 KW T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
 KW Toxoplasma oocyst; ss.
 XX
 OS Toxoplasma gondii.
 XX
 PN WO9932633-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-US027137.
 XX
 PR 19-DEC-1997; 97US-00994825.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Milhausen MJ, Lutz SB, Ng RK;
 XX P-PSDB; AAY29078.
 DR WPI; 1999-418930/35.
 DR
 PT New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
 PT infection caused by this microorganism.
 XX
 XX Example 15; Page 341-342; 381pp; English.
 PS
 CC The invention provides isolated Toxoplasma gondii nucleic acids that
 CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,

immunogenic proteins and antibodies to the proteins can be used to inhibit *T. gondii* oocyst shedding in a cat due to infection with *T. gondii*. They can be used for preventing *T. gondii* infection and for preventing the spread of *T. gondii* infection. They can also be used for detecting *T. gondii* infection. The detection method can be used to detect parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts such as *Cryptosporidium* oocysts and *Toxoplasma* oocysts

SQ Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;

| | | | |
|------------------------|-----------|---------------|------|
| Alignment Scores: | 1.58e-101 | Length: | 1785 |
| Pred. No.: | Score: | Matches: | 193 |
| | 1034.50 | Conservative: | 55 |
| Percent Similarity: | 77.3% | Mismatches: | 72 |
| Best Local Similarity: | 60.1% | Indels: | 1 |
| Query Match: | 61.3% | Gaps: | 1 |
| DB: | 2 | | |

US-09-390-846-2 (1-330) x AAX91434 (1-1785)

Qy 9 ArgProLYsIleAlaMetValGlySerGlyMetIleGlycylThrMetalAlaPheLeuCys 28
Db 109 AGAAAGAGGTGGCATGATGGCTCTGGCATGATTGGTCATATGGCTACCTGTGC 168

| | | | |
|----|-----|--|-----|
| Qy | 29 | SerLeuArgGluLeuGlyAspValValIleuPheAspValValProAsnMetProMetGly | 48 |
| Db | 169 | GCTTCCTCCGTGAGCTCGCTGACGTCGTCTCTACGATGTTGTTCAAAAGTATGCCCGAGGGT | 228 |

| Qy | 49 | LysAlaMetAspTleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly | 68 |
|----|-----|--|-----|
| Db | 229 | AAGGCTCTTGACCTGAGCCATGTGACCTCCGTGGTGCACCAACAGCTTTCGTCGCGTGCT | 288 |

Qy 69 Ser^{Asn}Ser^{Tyr}Glu---CysLeu^{ys}GlyAlaAspVal^{lle}Ile^{lle}ThrAla^{Gly}Ile 87
Db 289 GACTACTCTTACGAGCGCGCTCACCGGTGCGACTCGTTATGCTTACCGCGGTCTC 348

| Qy | 88 | ThrLysIleProClyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsn | 107 |
|----|-----|--|-----|
| | ... | ... | |
| Db | 349 | ACCAAGGTGCCGGGCAAGCCCGACTCCGAGTGGAGCCGAAACGATGTGCTCCGTTCAAC | 408 |

| | | | |
|----|-----|--|-----|
| QY | 108 | IleLysIleMetArgGluValGlyAlaAlaIleIysSerTyrCysproAsnAlaIleVal | 127 |
| Db | 409 | TCGAAGATCATTCGCGAGTCCGTCGAGACATCAAGAAGTACTGCCCCAGACCTTCATC | 468 |

| Qy | 128 | IleAsnIleThrAsnProLeuAspValMetValAlaAlaIleuGlnGluSerSerCysLeu | 147 |
|----|-----|---|-----|
| Db | 469 | ATCGTGGTCAACCAACCCGCTGGACGTGCATGGTCAAGGTCAATGTCGAGGCGTC | 528 |

| | | | |
|----|-----|--|-----|
| Qy | 148 | ProHisHisArgIleCysIleMetAlaGlyMetIleuAspSerArgPheArgMet | 167 |
| | | ... | |
| Db | 529 | CGACCAACATGATCTGCGGTATGGCCCTGCATGCTCGACTCTGTCGCTTCGCGCATAC | 588 |

| | | | |
|----|-----|--|-----|
| Qy | 168 | IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis | 187 |
| | | | |
| Db | 589 | GTGCGCAGCGGTGTCTGTCTCTCCCGCGAGCTCCAGGCCACCGTCTATCGGCACAC | 648 |

[illegible]

| | | | |
|----|-----|---|-----|
| Db | 709 | TTCATCAAGGAGCGCGGTAGTCACGGAGAAGCAGCTCGAGGAGATCGCTGACGACACCCAAA | 768 |
| Qy | 208 | PreVal1ysLyscyslytRip1letysGlnGluGluValAspAspIleValGlnLysThrLys | 227 |
| Qy | 208 | PreVal1ysLyscyslytRip1letysGlnGluGluValAspAspIleValGlnLysThrLys | 227 |

QY 228 valAlaGlyGlyIuIleValArgLeuLeuGlyGlnGlySerAlaIyrTrAlaProGly 244
::: :
769 GTGTCTGGCGGGAGATCGTCCGCTTCCTCGGCAGGGTTCGGTTACTACGCCCCCGCC 828
Db

D_b

829 GCATCCGCTGTGC CATGGCAACATCCTTCTTGAAACGACGAAAAGCGCGTCATCCCCGTGC 888

QY

248 AIAASeRAIIIEuInMeAlaGIuSerTy rLeuLysAspArgLysArgValMetValCys 267

QY 208 serCys.iyrLeuGnGlyGlnIlyrGlyValGlnAsnHisTyrLeuGlyValProCysVal 281

[illegible]

| | | | |
|----|------|-----|------|
| Qy | 328 | Ala | 328 |
| | | | |
| Db | 1069 | GCG | 1071 |

RESULT 3
AAX91435
ID AAX91435 standard; DNA; 1785 BP.

AC AAX91435;
XX
DT 24-SEP-1999 (first entry)

DE
XX
KW

KW Toxoplasma oocyst; 55.
XX
OS Toxoplasma gondii.
OS Toxoplasma gondii.

PN WO932633-A1.
XX
XX
PD 01-JUL-1999.
XX

PF 18-DEC-1998; 98WO-US027137.
XX
PR 19-DEC-1997; 97US-00994825.
XX

(HESK-) HESKA CORP.
PA
XX
PI
XX
XX
Milhausen MJ, Lutz SB, Ng RK;
.

DR WPI; 1999-418930/35.
XX New isolated *Toxoplasma gondii* nucleic acids used, e.g. to treat
PT infection caused by this microorganism
PT

XX
XX
XX The invention provides isolated Toxoplasma condi
XX nucleic acids that
XX Example 15; Page 342-344; 38tpp; English.
XX PS
XX CC

CC encode immunogenic polypeptides. The *T. gondii* nucleic acid molecules,
CC immunogenic proteins and antibodies to the proteins can be used to
CC inhibit *T. gondii* oocyst shedding in a cat due to infection with *T.*
CC *gondii*. They can be used for preventing *T. gondii* infection and for
CC *gondii*. They can be used for preventing *T. gondii* infection and for

CC preventing the spread of *T. gondii* infection. They can also be used for
CC detecting *T. gondii* infection. The detection method can be used to detect
CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
CC such as *Cryptosporidium* oocysts and *Toxoplasma* oocysts

XX
 SQ Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;
 Alignment Scores:

Score: NO.:
1:308-101
Length: 1785
Matches: 193
Percent Similarity: 55
Best Local Similarity: 60.1%
Mismatches: 72

| | | | | | |
|-----------|-----------------|---------|---|----------|----------|
| DB: | US-09-390-846-2 | (1-330) | x | AAx91435 | (1-1785) |
| Indexers: | 2 | | | | 1 |
| Gaps: | | | | | 1 |

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28

```

Db 109 AGAAGAAGTGGCGCATGATTGGCTCTGGCATGATTGGTGGCATATGGGCTACTCTGTC 168
Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
Db 169 GCTCTCCGTGAGCTCGCTGACGTGCTTCTCTACCATGTTGTCAAAAGGTATGCCGAGGCT 228
Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly 68
Db 229 AAGGCTCTTGACCTGAGCCATGTGACCTCCGTGGTGCACACCAACGTTTCGTCCTGCT 288
Qy 69 SerAsnSerTyGlu--CysLeuLysGlyAlaAspValValIleIleThrAlaGlyIle 87
Db 289 GAGTACTCTTACGAGCCGCTCACCCTGCGGACTCGCTTATCGTTACCGCCGGTCTG 348
Qy 88 ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsn 107
Db 349 ACCAAGGTGCCGGCAGCCGACTCCGAGTGGAGCGAAGCATCTGCTCCCGTTCAAC 408
Qy 108 IleLysIleMetArgGluValGlyAlaAlaIleLysSerTyGlyProAsnAlaPheVal 127
Db 409 TCGAAGATCATTCGCGAGATCGGTGAGAACATCAAGAGTACTGCCCCAGACCTTCATC 468
Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaIleGluGlnGluSerSerGlyLeu 147
Db 469 ATCGTGTGTCACCAACCCGCTGATGTCATGTCATGTCGAGGCCCTCTGGCGTC 528
Qy 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
Db 529 CCGACCAACATGATCTCGCGGTATGCGCTGTCATGTCGACTCTGCTGCGCTCCGCGATAC 588
Qy 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
Db 589 GTCCGCGACCGGCTGTCTCTCTCCCGCACGTCCAGGCCACCGTCATCGGCACACAC 648
Qy 188 GlyAspHisMetValProLeuSerArgTyAlaThrValAnGlyIleProLeuSerGlu 207
Db 649 GCGGACTCATGTCCTCCGCTTGTCCGGTACATTTACCGTGAACGACTCCCATCCGATCAGAG 708
Qy 208 PheValLysLysGlyTrpIleLysGlnGluValAspIleValGlnLysThrLys 227
Db 709 TTTATCAAGGACGGCGTAGTCACGAGAGAGAGCTCGAGGAGATCGCTGAGCACACCAA 768
Qy 228 ValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyThrAlaProGly 247
Db 769 GTGTCTGCGCGAGATCGCTCTCTCCGCGCAGGGTTCCGCTTACTACGCCCCCGCC 828
Qy 248 AlaSerAlaIleGlnMetAlaGluSerTyLeuLysAspArgLysArgValMetValCys 267
Db 829 GCATCCGCTGTCCCATGCGCAACATCTCTTGAACGACGAAGAGCGGTCTATCCCGTGC 888
Qy 268 SerCysTyLeuGlnGlyGlnTyGlyValGlnHisIstTyLeuGlyValProCysVal 287
Db 889 AGTGTGTACTGCAACGGAGAGTACGGCTTGAAGGACATGTTTCATTGGTCTCCCGCGCTC 948
Qy 288 IleGlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGln 307
Db 949 ATTGAGGCGCGGATCGAGCGCTCATCGAGCTCGAGCTGAACGAGGAGGAGAAGAAG 1008
Qy 308 GluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaAlaLeuAsp 327
Db 1009 CAGTCCAGAGTCTCGTCGACGAGTCAATGGCGCTCAACAGGCGGTGCTGCTTTCAG 1068
Qy 328 Ala 328
Db 1069 GCG 1071

```

RESULT 4

AAS42758

ID AAS42758 standard; cDNA; 1785 BP.

XX

AC AAS42758;

XX

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Dt 17-DEC-2001 (first entry)
Xx T. gondii cDNA encoding immunogenic protein PMGIS65.
Xx Immunogenic protein; oocyst; faeces; ss; enteric apicomplexa oocyst;
Xw Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;
Xw oocyte shedding.
Xx Toxoplasma gondii.
Xs US2001014447-A1.
Xn 16-AUG-2001.
Xx 18-DEC-1998; 98US-00216393.
Xx 19-DEC-1997; 97US-00994825.
Xx (MILH/) MILHAUSEN M J.
Xx Milhausen MJ;
Xx WPI; 2001-529100/58.
Xx P-PSDB; AAU25549.
Xx Detecting parasite oocysts or cysts in feces, comprises eluting DNA from
Xx sample into aqueous solution by heating, amplifying DNA with primers
Xx specific for oocysts or cysts being detected, and detecting amplification
Xx product.
Xx Example 15; Page 165-166; 188pp; English.
Xs The invention relates to detection of parasite oocysts or cysts in a
Cc faeces sample comprising contacting the sample with a solid support,
Cc drying and then washing the sample with an aqueous wash solution, adding
Cc an aqueous elution solution and eluting DNA from the sample by heating
Cc and amplifying by PCR oocyst/cyst-specific DNA and detecting the
Cc amplification products. The method is useful for detecting parasite
Cc oocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts
Cc or Toxoplasma oocysts, or for detecting parasite cysts e.g. Giardia
Cc cysts. The method is also useful for developing vaccines to prevent
Cc oocyte shedding in cats. The present sequence encodes an immunogenic
Cc protein from Toxoplasma gondii.
Xx SQ Sequence 1785 BP; 393 A; 490 C; 503 G; 399 T; 0 U; 0 Other;

```

Alignment Scores:

```

Pred. No.: 1.58e-101 Length: 1785
Score: 1034.50 Matches: 193
Percent Similarity: 77.3% Conservative: 55
Best Local Similarity: 60.1% Mismatches: 72
Query Match: 61.3% Indels: 1
DB: 4 Gaps: 1

```

US-09-390-846-2 (1-330) x AAS42758 (1-1785)

```

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
Db 109 AGAAGAAGTGGCGCATGATTGGCTCTGGCATGATTGGTGGCATATGGGCTACTCTGTC 168
Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
Db 169 GCTCTCCGTGAGCTCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228
Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly 68
Db 229 AAGGCTCTTGACCTGAGCCATGTGACCTCCGTGGTGCACACCAACGTTTCGTCCTGCT 288
Qy 69 SerAsnSerTyGlu---CysLeuLysGlyAlaAspValValIleIleThrAlaGlyIle 87
Db 289 GAGTACTCTTACGAGCGCGCTCACCCTGCGGACTCGCTTATCGTTACCGCCGGTCTG 348
Qy 88 ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsn 107

```


KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; gene; ss.
 XX
 XX
 OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAO/Y) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 XX for expression of a polynucleotide encoding a polypeptide from a
 XX microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 41525; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 960 BP; 170 A; 325 C; 311 G; 154 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 3.06e-85 | Length: | 960 |
| Score: | 880.50 | Matches: | 173 |
| Percent Similarity: | 70.7% | Conservative: | 54 |
| Best Local Similarity: | 53.9% | Mismatches: | 89 |
| Query Match: | 52.2% | Indels: | 5 |
| DB: | 13 | Gaps: | 1 |

US-09-390-846-2 (1-330) x ADR43087 (1-960)

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28

|||||

| | | | |
|----------|-------------|--|-----|
| Db | 7 | CGAAGAAGATCGCGCTGATCGGCTCGCGCATGATCGTGGCACCTTCGGCACCTCGCT | 66 |
| Qy | 29 | SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly | 48 |
| Db | 67 | GCAATCAAGAACTGGCGGATATCGTCTGTGCATTTCCGAGGGCAGCCCGCAGGCG | 126 |
| Qy | 49 | LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly | 68 |
| Db | 127 | AGGCGCTCGACATCGACAGTCCGGACCGGTCGAGGCTTCGATGCGCAACCTCAAGGC | 186 |
| Qy | 69 | SerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr | 88 |
| Db | 187 | GCGAACAGCTACGAGGACATTGGCGGCGCGCATCTGTCATCGTCACCGCGGTATCCG | 246 |
| Qy | 89 | LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle | 108 |
| Db | 247 | CGCAAGCGCGGC-----ATGAGCGCGGACGATCTTCTCAAGACCAACCTG | 291 |
| Qy | 109 | LysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValIle | 128 |
| Db | 292 | GGCGTATGAAGCGGTGGGAGGCGATCGCCGCGCACCGCCCGCGGTTCGTGATC | 351 |
| Qy | 129 | AsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro | 148 |
| Db | 352 | TGCATCACCACCGCTCGACCGCATGCTGTGGCGCTGCGGAGTTCTCGGCGCTGCG | 411 |
| Qy | 149 | HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle | 168 |
| Db | 412 | CACAGAAAGTCTGCGCGCATGCGCGGTCTGCTGCGCGCGCTTCGCGCACTTCCTC | 471 |
| Qy | 169 | AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly | 188 |
| Db | 472 | GCCAGGAATTCACGCTCTCGTTCGAGACGTCACCGCTTCGTGCTGGCGGACACGC | 531 |
| Qy | 189 | AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe | 208 |
| Db | 532 | GACACCATGCTCCGGTATCGAGTATTCGACCGCTCGCGCATCCCGTTCGCGACCTG | 591 |
| Qy | 209 | ValLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLysVal | 228 |
| Db | 592 | ATCAAGATGGCTGGTCCACCCAGGAGCGCATCGCCGCTTCGTGGCGGACCGCTCG | 651 |
| Qy | 229 | AlaGlyGlyIleValArgLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla | 248 |
| Db | 652 | GGCGGCGGAGATCGTCCGCTCTCAAGACCGCTCGCGCTATTCGCGCGGCCACC | 711 |
| Qy | 249 | SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer | 268 |
| Db | 712 | AGCGGATCGGATGGCGGAGAGCTATCTGAAGGACAAAGACGCTCTTCCTGTGCT | 771 |
| Qy | 269 | CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle | 288 |
| Db | 772 | CGCACCTTCACCGGCGGATGCGGCTGCTGATGCTGCGCGCTGCGGATCGCTATC | 831 |
| Qy | 289 | GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnArgGlnGlu | 308 |
| Db | 832 | GCGAAGGACGCGTGGCGGATGTCGATGATGAGCTGACGCGCACCGCGGAGCAGAT | 891 |
| Qy | 309 | LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaAlaLeuAspAla | 328 |
| Db | 892 | TTCGACGCTCGGTGATGCGGTCAAGGAAGTGGTGGCAGCATGCAAGTTCGATCGAC | 951 |
| Qy | 329 | Ser 329 | |
| Db | 952 | TCG 954 | |
| RESULT 9 | | | |
| ID | ADS59454 | standard; cDNA; 957 BP. | |
| AC | ADS59454; | | |
| XX | 02-DEC-2004 | (first entry) | |

XX Bacterial polynucleotide #11441.

DE Recombinant DNA construct; transformed plant; improved plant property;

XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polynucleotide; gene; ss.

XX Bacteria.

OS US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAO/Y) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 35128; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polynucleotide used in

CC the scope of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 957 BP; 182 A; 307 C; 273 G; 195 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1.74e-84 | Length: | 957 |
| Score: | 873.50 | Matches: | 167 |
| Percent Similarity: | 72.3% | Conservative: | 60 |
| Best Local Similarity: | 53.2% | Mismatches: | 82 |
| Query Match: | 51.7% | Indels: | 5 |
| DB: | 13 | Gaps: | 1 |

US-09-390-846-2 (1-330) x ADS59454 (1-957)

| | | | |
|----|-----|--|-----|
| QY | 9 | ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys | 28 |
| DB | 7 | CGCAAAAAATTGCACATTATTGGTTCTGGCATGATCGCGCGCACGCTGGCGCATCTCGCC | 66 |
| QY | 29 | SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly | 48 |
| DB | 67 | AGCCTGAAGGAACATGGCGATATCTCTTCGACATCGCGCAGCGCATCCCGAGGGC | 126 |
| QY | 49 | LysAlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrValTyrGly | 68 |
| DB | 127 | AAGGCTCTGGATATTGCCACGTCGCCCGCGGTGAAGGCTTCAATGCAAGCTCTCCGC | 186 |
| QY | 69 | SerAsnSerTyrGluCysLeuGlyAlaAspValValIleThrAlaGlyIleThr | 88 |
| DB | 187 | GCTTCGATTAACGCGCCATCGAAGCGCAGACGCTCTGCATCGTCACCGAGGTGTCGC | 246 |
| QY | 89 | LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle | 108 |
| DB | 247 | CGCAAGCCCGC-----ATGAGCCCGCATGATCTTCTTGGCATCAACCTC | 291 |
| QY | 109 | LysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheValIle | 128 |
| DB | 292 | AAGTCTATGGACAGTGGCGCGGCATCAAGAAATATGCTCCGAACGCTTTCGTGATC | 351 |
| QY | 129 | AsnIleThrAsnProLeuAspValMetValAlaLeuGlnGlnSerSerGlyLeuPro | 148 |
| DB | 352 | TGCATCACCAACCCGCTCGACGCCATGCTTGGCGCTGCAGAGTTCTCCGCCCTGCG | 411 |
| QY | 149 | HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle | 168 |
| DB | 412 | AAGAACAAAGTTCGCGCATGCTGGCGTTCTCGACAGCGACGCTTCGCTGTTCCT | 471 |
| QY | 169 | AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly | 188 |
| DB | 472 | CCCAAGAAATTCAACGTTTCGTCAGACGTCACCGCTTCGTCTCGCGGTTCATGCG | 531 |
| QY | 189 | AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe | 208 |
| DB | 532 | GACACCATGTTGCGCTCGCCCGTTATTCACCGTTGCGCGGTTCGCTTACCGATCTC | 591 |
| QY | 209 | ValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLysVal | 228 |
| DB | 592 | GTCAGATGGGCTGGTTGACCGCGAACGCTTTCAGACAGATCATCCAGCGACCGTGAC | 651 |
| QY | 229 | AlaGlyGlyGluIleValArgLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla | 248 |
| DB | 652 | GGCGCGCGGAAATCGTCGCGCTCTTGAAGACCGGCTCGGCTATTACGCGCGCGCT | 711 |
| QY | 249 | SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer | 268 |
| DB | 712 | TCGCTATCGAAATGGCGCATCTACTCAAGACCAAGAGCGGTTCTCGCGCTGCT | 771 |
| QY | 269 | CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle | 288 |
| DB | 772 | GCCACACCTTCGGGCCAGTATGGGTAGACGACATGATGTCGCGGTGCCCATCATC | 831 |
| QY | 289 | GlyClyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu | 308 |
| DB | 832 | GGTCCGCGGCTATCGAGCGCGCTCATCGATCGAACTGAACAAGGAAGAGAGCGGCC | 891 |
| QY | 309 | LeuGlnGlySerIleAspGluValLysGluMetGlnLysAla | 322 |
| DB | 892 | TTCCAGAAATCCGTCGCGCGCTGTCGCTGGTCTTTCGGAAGCC | 933 |

RESULT 10

| | | |
|----|-------------|-------------------------|
| ID | ADS62502 | standard; cDNA; 960 BP. |
| XX | ADS62502 | |
| AC | ADS62502; | |
| XX | 02-DEC-2004 | (first entry) |
| DT | | |
| XX | | |

DE Bacterial polynucleotide #14489.

KW Recombinant DNA construct; transformed plant; improved plant property;

XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polynucleotide; gene; ss.

XX Bacteria.

XX OS

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAO Y.) CAO Y.

XX (HINKLE G J.) HINKLE G J.

XX (SLATER S C.) SLATER S C.

XX (CHEN X.) CHEN X.

XX (GOLDMAN B S.) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

DR New recombinant DNA construct comprising a promoter positioned to provide

XX for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

PT Claim 1; SEQ ID NO 38176; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polynucleotide used in

CC the scope of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 1-75e-84 | Length: | 960 |
|------------------------|----------|---------------|-----|
| Score: | 873.50 | Matches: | 167 |
| Percent Similarity: | 72.3% | Conservative: | 60 |
| Best Local Similarity: | 53.2% | Mismatches: | 82 |
| Query Match: | 51.7% | Indels: | 5 |
| DB: | 13 | Gaps: | 1 |

US-09-390-846-2 (1-330) x ADS62502 (1-960)

RESULT 11

ADS62887

ID ADS62887 standard; cDNA; 960 BP.

XX ADS62887;

AC ADS62887;

XX 02-DEC-2004 (first entry)

XX Bacterial polynucleotide #14874.

DE

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; gene; ss.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAO//) CAO Y.
 PA (HINK//) HINKLE G J.
 PA (SLAT//) SLATER S C.
 PA (CHEN//) CHEN X.
 PA (GOLD//) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 DR
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 960 BP; 184 A; 307 C; 274 G; 195 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,75e-84 Length: 960
 Score: 873.50 Matches: 167
 Percent Similarity: 72.3% Conservative: 60
 Best Local Similarity: 53.2% Mismatches: 82
 Query Match: 51.7% Indels: 5
 DB: 13 Gaps: 1
 US-09-390-846-2 (1-330) x ADS62887 (1-960)
 Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28

Db 7 CGCAAAAATTCACCTTATTGGTTCTGGCATGATCGCGGCACGCTCGCGCATCTCGCC 66
 Qy SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
 Db 67 AGCTCGTAGGAACATGGCGGATATCGTCTCTTCGACATCGCGCGCATCCCGCAGGCG 126
 Qy LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
 Db 127 AAGGTCCTGGATATTGCCACGTCGCGCGCGGTTCGAAGGCTTCAATGCAAAAGCTCTCCGCG 186
 Qy 69 SerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr 88
 Db 187 GCTTCGGATTACGCGCCATCGAAGCGCACGCTCTGCATCGTCACCGAGGTCTCGCC 246
 Qy 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
 Db 247 CGCAAGCCCGCG-----ATGAGCCCGATGATCTTCTTGGCATCAACCTC 291
 Qy 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValIle 128
 Db 292 AAGGTCATGGAACAGGTGCGCGCGCATCAAGAAATATGCTCCGACGCTTTCGTGATC 351
 Qy 129 AsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeuPro 148
 Db 352 TGCATCACCAACCCCGCTCGACGCCATGCTTGGCGCTGCAGAAAGTTCTCGCGCTCGCG 411
 Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMetIle 168
 Db 412 AAGAACAGGTCTGCGCATGCTGGCGGTCTTCGACAGCGACGCTTTCGCTGTCTCT 471
 Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
 Db 472 GCCGAAGAATTCACGTTTCTGCTCCAGGACGTCACCGCTTCTGTTCTCGCGGTCTATGCG 531
 Qy 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe 208
 Db 532 GACACCATGGTGGCGCTCGCGCTTATTCACCGTTCGCGCGGTTCGCTTACCGATCTC 591
 Qy 209 ValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLysVal 228
 Db 592 GTCAAGTGGCTGGTTGACCGCGCAACGCTTTCGAGCAGATCATCCAGCGCACCGCTGAC 651
 Qy 229 AlaGlyGlyIleValValArgLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
 Db 652 GCGCGCGGGAATCGTGGCGCTCTTGAAGACCGCTCTGAGCCTATTACGCGCGCGCT 711
 Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
 Db 712 TCGGCTATCGAAATGGCGAATCTTACCTCAAGGACACGAGCGGCTTCTCGCGCTGCT 771
 Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
 Db 772 GCCACCTTTCGCGCGCGATGTCGCGTACGACATGATGTCGCGGTGCCACCATCATC 831
 Qy 289 GlyGlyArgGlyValGluLysIleLeuLeuGluLeuThrAlaGlnGluArgGlnGlu 308
 Db 832 GGTCCGCGCGGTATCGAGCGGTCTATCGAGATCGAATGACACTGACACAGGAAGAGACGCC 891
 Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAla 322
 Db 892 TTCCAGAAATCCGTGCGCGCTGTCGCTGCTTTCGGAAGCC 933
 RESULT 12
 ID ADT45997 standard; cDNA; 933 BP.
 XX
 AC ADT45997;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polynucleotide #20748.
 XX

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmoesis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; gene; ss.
 XX
 OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 XX for expression of a polynucleotide encoding a polypeptide from a
 XX microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 35747; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 XX promoter functional in a plant cell, where the promoter is positioned to
 XX provide for expression of a polynucleotide encoding a polypeptide from a
 XX microbial source. The invention also relates to a transformed plant
 XX comprising the recombinant DNA construct and a method of producing a
 XX transformed plant having an improved property. The plant is a crop plant
 XX such as maize or soybean. The method of producing a transformed plant
 XX having an improved property comprises transforming a plant with the
 XX recombinant DNA construct and growing the transformed plant, where the
 XX polynucleotide or polypeptide is useful for improving plant properties.
 XX The recombinant DNA construct is useful for producing plants with
 XX improved plant properties, e.g. improved cold, heat or drought tolerance,
 XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 XX increased resistance to plant disease, better growth rate by modification
 XX of the cell cycle pathway with plant growth regulators, increased rate of
 XX homologous recombination, modified seed oil or protein yield and/or
 XX content, improved yield by modification of carbohydrate, nitrogen or
 XX phosphorus use and/or uptake, by modification of photosynthesis or by
 XX providing improved plant growth and development under at least one stress
 XX condition, improved lignin production or improved galactomannan
 XX production. This sequence represents a bacterial polynucleotide used in
 XX the scope of the invention. Note: The sequence data for this patent did
 XX not form part of the printed specification but was obtained in electronic
 XX format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 969 BP; 174 A; 310 C; 309 G; 176 T; 0 U; 0 Other;

XX Alignment Scores:

| Pred. No.: | 3.11e-83 | Length: | 969 |
|------------------------|----------|---------------|-----|
| Score: | 862.00 | Matches: | 174 |
| Percent Similarity: | 70.8% | Conservative: | 56 |
| Best Local Similarity: | 53.5% | Mismatches: | 87 |
| Query Match: | 51.1% | Indels: | 8 |
| DB: | 13 | Gaps: | 2 |

XX US-09-390-846-2 (1-330) x ADS60073 (1-969)

Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28

Db 7 CGCAACAGATAGCGCTTATCGGCTCGGGCATGATCGCGGCACGCTGGCCCATGATC 66

| | | | |
|-----------|----------------------------------|---|-----|
| Qy | 29 | SerLeuArgGluLeuGlyAspValValPheAspValValProAsnMetProMetGly | 48 |
| Db | 67 | GGCTCAAGGACCTCGCGGAGCTGCTGTGATATGCCGAGGGTATTCGCCAAGGC | 126 |
| Qy | 49 | LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly | 68 |
| Db | 127 | AAGGGGCTCATATCGCGCAGTCGTCGCGGTTCGATTCGCGCTGACCGGC | 186 |
| Qy | 69 | SerAsnSerTyrgluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr | 88 |
| Db | 187 | GTCAACGACTATGCGCGCATCGAGGGTGGCGGCTGTCATCGTTACAGCGGGGTGCGC | 246 |
| Qy | 89 | LysIleProGlyLysSerAspLysGluTrpSerIleMetAspLeuLeuProValAsnIle | 108 |
| Db | 247 | CGCAAGCCTGGC-----ATGAGCGCGCAGCATCTGCTGGGATCAACCTC | 291 |
| Qy | 109 | LysIleMetArgGluValGlyAlaIleLysSerTyrgCysProAsnAlaPheValIle | 128 |
| Db | 292 | AAGTCTATGGAACTGGCGGCGCGGCTGCTGAAGATATGCCGCCAAGGCTTCGTATC | 351 |
| Qy | 129 | AsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro | 148 |
| Db | 352 | TGCATCAACCAATCGCTCGAGCCCATGCTGTGGGCGCTGCAGAAAGTTTCCGCGCTGCC | 411 |
| Qy | 149 | HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle | 168 |
| Db | 412 | AAGACCATGTCGTCGCGCATCGCGGCTGCTGCACAGCGCGCTTCCTGCTATTCCTG | 471 |
| Qy | 169 | AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly | 188 |
| Db | 472 | GCCGAGGAATTCAAAGTTCGCTCGTGCAGGAGCTCACCGCTTCGTGCTGGCGGCACGCG | 531 |
| Qy | 189 | AspHisMetValProLeuSerArgTyrgAlaThrValAsnGlyIleProLeuSerGluPhe | 208 |
| Db | 532 | GATTCATGTCGCGATGATCGGCTACTCGACGCTATCGGCGCATCCGCTGCCCGACCTC | 591 |
| Qy | 209 | ValLysLysGlyTrpIleLysGlnGluValAspIleValGlnLysThrLysVal | 228 |
| Db | 592 | GTCAAGATGGGCTCGACCTCGAAGGAGAAGCTCCAGCAGATCGTCCAGCGCACCGCTGAT | 651 |
| Qy | 229 | AlaGlyGlyIleValArgLeuGlyGlnGlySerAlaTyrgAlaProGlyAla | 248 |
| Db | 652 | GGCGGCGCGGAGATCGTCGCGCTCTCAAGACCGGCTCGGCTATTCGCGCGCGCGGCC | 711 |
| Qy | 249 | SerAlaIleGlnMetAlaGluSerTyrgLysAspArgLysArgValMetValCysSer | 268 |
| Db | 712 | TCGCGGATTCGCTATGGCGGATCTCTACTCAAGGACAAAGACCGCGTCTGCTGCTGCTGCT | 771 |
| Qy | 269 | CysTyrgLeuGlnGlyIleTyrgIleValGlnAsnHisTyrgLysValProCysValIle | 288 |
| Db | 772 | GCCACCTTTTCGCGCCAGTATGGCTCAAGGGCACCTATGTCGCGCTCCCGCTGGTATC | 831 |
| Qy | 289 | GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu | 308 |
| Db | 832 | GGCGCGCGCGCTCGAGCGCATCATGAGTATTCATCAACAGAGCGGACACAAATATG | 891 |
| Qy | 309 | LeuGlnGlySerIleAspGluValLysGluMetGlnLysAla-----IleAlaAla | 325 |
| Db | 892 | TTGAGAGATTCGGTGGCGACCGTGCAGGCGCTGCAGGAGCTCGGCTCAAGATCGCGCG | 951 |
| Qy | 326 | LeuAspAlaSerLys | 330 |
| Db | 952 | CAGCTCGCTTCGAG | 966 |
| RESULT 14 | | | |
| ID | ADT42328 standard; cDNA; 963 BP. | | |
| XX | ADT42328 | | |
| XX | AC ADT42328; | | |
| XX | DT 02-DEC-2004 (first entry) | | |
| XX | | | |

XX 02-DEC-2004 (first entry)
 XX Bacterial polynucleotide #8013.
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polynucleotide; gene; ss.
 XX Bacteria.
 XX US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 XX (CAO Y.) CAO Y.
 XX (HINKLE G J.) HINKLE G J.
 XX (SLATER S C.) SLATER S C.
 XX (CHEN X.) CHEN X.
 XX (GOLDMAN B S.) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX Claim 1; SEQ ID NO 31700; 122pp; English.
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polynucleotide used in
 CC the scope of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX Sequence 960 BP; 169 A; 311 C; 325 G; 155 T; 0 U; 0 Other;
 XX Alignment Scores:
 XX Pred. No.: 8,86e-82 Length: 960
 XX Score: 848.50 Matches: 163
 XX Percent Similarity: 70.7% Conservative: 64
 XX Best Local Similarity: 50.8% Mismatches: 89
 XX Query Match: 50.3% Indels: 5
 XX DB: 13 Gaps: 1

US-09-390-846-2 (1-330) x ADS56026 (1-960)
 Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeuCys 28
 Db 7 AGACCCAAAGATTGGCTGCTGCGGGGCGAGATCGGCGGCAGCTCGCCCATCTCGCC 66
 Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
 Db 67 GCGATCAAGGAATCGGGCGAGCTGCTGTTGCATCGCCGAAGGCACCCCTCAGGGC 126
 Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly 68
 Db 127 AAGGCTCTGGACATCGCGCAATCGGGCCCTCGGAAGGCTTCGAGCGCGTGTGAAGGGC 186
 Qy 69 SerAsnSerTyrgluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr 88
 Db 187 GCGAACAGCTACGAAGAGATCGCGGGCGCGACGCTCTGCATCGTGACCGGGGCTGCGC 246
 Qy 89 LysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuProValAsnIle 108
 Db 247 CGCAAGCCCGGC-----ATGAGCGCGAGCAGCTGATCGGCATCAACCTC 291
 Qy 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyrgluCysProAsnAlaPheValIle 128
 Db 292 AAGGTGATGAATCGGTGCGGAGGATCAAGGCCCATCGCGCGAAGCGCTTCGTGATC 351
 Qy 129 AsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeuPro 148
 Db 352 TGCATCACCAACCCGCTCGACCGCATGGTCTGGGGCGCTGCAGCAATTCCTGGGGCTGCGC 411
 Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
 Db 412 GCGAGAAGGTGGGGCGGTGCGGGCGGTCTCGACTCGGGCGCTTCGGCATTTCTCTG 471
 Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
 Db 472 TCGGTGAGTTCAACGCTCTCGATCGCGACGTGACGGCTTCGTCTCTGGGGCGGCATGCG 531
 Qy 189 AspHisMetValProLeuSerArgTyrgluAlaThrValAsnGlyIleProLeuSerGluPhe 208
 Db 532 GACAGATGGTGGCGCTGCTCGCTACTCGACGGTGGCGGCATCCCGCTCCCGCATCTC 591
 Qy 209 ValLysLysGlyTrpIleLysGlnGluGluValAspAspIleValGlnLysThrLysVal 228
 Db 592 GTGCAGATGGGTGGACCCAGCAGAGAGCTCCAGCAGATCGTGCGAGCGCACCGGTGAC 651
 Qy 229 AlaGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrgluAlaProGlyAla 248
 Db 652 GCGCGCGCGAGATCGTGGGGCTCTGTAAGACCGGCTCGGCTTCTACGCGCGCGCCACC 711
 Qy 249 SerAlaIleGlnMetAlaGluSerTyrgluLysAspArgLysArgValMetValCysSer 268
 Db 712 TCGGCCATCGAGTGGCGGAAGCCTATCTCAAGACACAGAGCGCTGCTGCTCCCTCGCGC 771
 Qy 269 CysTyrgluGlnGlyLntyrGlyValGlnAsnHisTyrgluGlyValProCysValIle 288
 Db 772 GCCTATGTGACGGCGCTTCGGCTGACCGCATGTATGTGGGGCGTGGCCACCATCATC 831
 Qy 289 GlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308
 Db 832 GCGCGCGCGGATCGAGAGATCGTGCATCAAGCTCAACGACGACGACGACGACGCGATG 891
 Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeuAspAla 328
 Db 892 TTCGACCAAGTCGGTCAATCGGGTGAAGGGCGCTCGTGGAGGCTTGAAGGGCGATCGACTCC 951
 Qy 329 Ser 329
 Db 952 TCG 954

Search completed: March 3, 2006, 00:00:56

Job time : 118 secs



GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 23:46:13 ; Search time 4597 Seconds
(without alignments)
4080.561 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVFEKTRPKIAWVGSGMI.....GSIDEVKEMOKATAALDASK 330

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abs/ABSSWEB spool/US09390846/runat_02032006 104230 4827/app query fasta_1
-DB-GenEmbl -EMFT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORES=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p
-USER=US09390846 @CGN 1 1 7415 @runat_02032006 104230 4827 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WAE TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*

1: gb_ba:*

2: gb_in:*

3: gb_env:*

4: gb_ov:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pr:*

9: gb_to:*

10: gb_sts:*

11: gb_ey:*

12: gb_un:*

13: gb_vi:*

14: gb_htg:*

15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 1688 | 100.0 | 1567 | 2 AY143388 | AY143388 Eimeria a |
| 2 | 1398 | 82.8 | 1411 | 2 AY143390 | AY143390 Eimeria m |
| 3 | 1266 | 75.0 | 1876 | 2 AY143389 | AY143389 Eimeria t |

| | | | | | | |
|----|--------|------|--------|----|-------------|---------------------|
| 4 | 1072 | 63.5 | 2593 | 2 | TGU23207 | U3207 Toxoplasma |
| 5 | 1041.5 | 61.7 | 1822 | 2 | TGU35118 | U35118 Toxoplasma |
| 6 | 1034.5 | 61.3 | 1785 | 6 | AR279170 | AR279170 Sequence |
| 7 | 1034.5 | 61.3 | 1785 | 6 | AR279171 | AR279171 Sequence |
| 8 | 905.5 | 53.6 | 951 | 2 | AY650028 | AY650028 Toxoplasma |
| 9 | 905.5 | 53.6 | 951 | 2 | AY972525 | AY972525 Toxoplasma |
| 10 | 889.5 | 52.7 | 1839 | 1 | RLAJ2750 | A002750 Rhizobium |
| 11 | 889 | 52.7 | 1350 | 2 | AB112429 | AB112429 Babesia b |
| 12 | 881 | 52.2 | 951 | 2 | DQ060151 | DQ060151 Plasmodiu |
| 13 | 880.5 | 52.2 | 31047 | 1 | EX897699_19 | Continuation (20 o |
| 14 | 876.5 | 51.9 | 11111 | 1 | AE009456 | AE009456 Brucella |
| 15 | 873.5 | 51.7 | 963 | 1 | AF322647 | AF322647 Sinorhizo |
| 16 | 873.5 | 51.7 | 10956 | 1 | AE009211 | AE009211 Agrobacte |
| 17 | 873.5 | 51.7 | 11683 | 1 | AE008177 | AE008177 Agrobacte |
| 18 | 873.5 | 51.7 | 81384 | 1 | EX897700_15 | Continuation (16 o |
| 19 | 873.5 | 51.7 | 333800 | 1 | SMES91792 | AL591792 Sinorhizo |
| 20 | 868.5 | 51.5 | 110000 | 1 | AE017223_18 | Continuation (19 o |
| 21 | 868 | 51.4 | 110000 | 1 | BA000040_04 | Continuation (5 of |
| 22 | 863.5 | 51.2 | 110000 | 1 | AE04291_18 | Continuation (19 o |
| 23 | 862.5 | 51.1 | 349315 | 1 | EX572593 | EX572593 Rhodopseu |
| 24 | 862 | 51.1 | 110000 | 1 | BA000012_34 | Continuation (35 o |
| 25 | 851.5 | 50.4 | 963 | 1 | AY181040 | AY181040 Methylola |
| 26 | 851.5 | 50.4 | 110000 | 1 | CP000031_03 | Continuation (4 of |
| 27 | 850.5 | 50.4 | 8617 | 1 | AE006023 | AE006023 Caulobact |
| 28 | 847 | 50.2 | 898 | 2 | AY486060 | AY486060 Plasmodiu |
| 29 | 838.5 | 49.7 | 13627 | 1 | AE008614 | AE008614 Rickettsi |
| 30 | 835 | 49.5 | 898 | 2 | AY486059 | AY486059 Plasmodiu |
| 31 | 831.5 | 49.3 | 951 | 2 | AB122147 | AB122147 Plasmodiu |
| 32 | 831.5 | 49.3 | 951 | 2 | AF251291 | AF251291 Plasmodiu |
| 33 | 831.5 | 49.3 | 951 | 2 | PFALDH | M3720 Plasmodium |
| 34 | 831.5 | 49.3 | 110000 | 14 | PFMAL13_10 | Continuation (11 o |
| 35 | 831.5 | 49.3 | 318221 | 14 | PFMAL13P3 | AL049184 Plasmodiu |
| 36 | 829.5 | 49.1 | 312430 | 1 | RPIX02 | AJ23271 Rickettsi |
| 37 | 826.5 | 49.0 | 110000 | 1 | AE017197_04 | Continuation (5 of |
| 38 | 825.5 | 48.9 | 110000 | 1 | CP000053_06 | Continuation (7 of |
| 39 | 810.5 | 48.0 | 220559 | 1 | AE017260 | AE017260 Wolbachia |
| 40 | 808.5 | 47.9 | 2210 | 15 | BBU00676 | UB0676 Botryococcu |
| 41 | 808.5 | 47.9 | 110000 | 1 | AE017321_03 | Continuation (4 of |
| 42 | 807.5 | 47.8 | 951 | 2 | AF323520 | AF323520 Plasmodiu |
| 43 | 807 | 47.8 | 898 | 2 | AY486058 | AY486058 Plasmodiu |
| 44 | 806.5 | 47.8 | 110000 | 1 | AE017180_15 | Continuation (16 o |
| 45 | 806.5 | 47.8 | 110000 | 1 | AE017180_16 | Continuation (17 o |

ALIGNMENTS

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| RESULT 1 | AY143388 | 1567 bp | linear | INV 18-MAY-2004 |
| LOCUS | Eimeria acervulina | lactate dehydrogenase (LDH) mRNA, complete cds. | | |
| DEFINITION | AY143388 | | | |
| ACCESSION | AY143388.1 | GI:25989636 | | |
| VERSION | Eimeria acervulina | | | |
| KEYWORDS | Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae; | | | |
| SOURCE | Schaap, D., Arts, G., Kroese, J., Niesse, R., Roosmalen-Vos, S.V., Spreeuwenberg, K., Kuiper, C.M., Beek-Verhoeven, N.V.D., Kok, J.J., Kneitel, R.M.A. and Vermeulen, A.N. | | | |
| ORGANISM | An Eimeria vaccine candidate appears to be lactate dehydrogenase; Characterization and comparative analysis | | | |
| REFERENCE | Parasitology 128 (6), 603-616 (2004) | | | |
| AUTHORS | 2 (bases 1 to 1567) | | | |
| TITLE | Schaap, D.C. | | | |
| JOURNAL | Characterization and cloning of lactate dehydrogenase from three | | | |
| REFERENCE | Eimeria species | | | |
| AUTHORS | Unpublished | | | |
| TITLE | 3 (bases 1 to 1567) | | | |
| JOURNAL | Kok, H.J., van den Boogaart, P., Vermeulen, A.N. and Schaap, D.C. | | | |
| REFERENCE | Direct Submission | | | |
| AUTHORS | Submitted (20-AUG-2002) Parasitology R&D, Intervet, Wim de | | | |
| TITLE | | | | |

| | | | |
|---|--|---|-----|
| Korverstraat, Boxmeer 5830AA, The Netherlands | | | |
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| ORIGIN | | | |
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| Pred. No.: | 1.76e-133 | | |
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| Percent Similarity: | 100.0% | | |
| Best Local Similarity: | 100.0% | | |
| Query Match: | 100.0% | | |
| DB: | 2 | | |
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| Qy | 1 | MetAlaValPheGluLysAsnThrArgProLysIleAlaMetValGlySerGlyMetIle | 20 |
| Db | 227 | ATGCGCGTCTTCGAGAAGAAATACACGCCCAAGATTGCTATGTTGGGCTCCGGTATGATT | 286 |
| Qy | 21 | GlyGlyThrMetAlaPheLeuCySerLeuArgGluLeuGlyAspValValPheAsp | 40 |
| Db | 287 | GGAGGCACCATGGCTTCTTGTCGAGCTTGAGGAATCGGAGATGTTGTCTCTTCGAC | 346 |
| Qy | 41 | ValValProAsnMetProMetGlyLysAlaMetAspIleSerHisAsnSerSerValVal | 60 |
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| Qy | 61 | AspThrGlyIleThrValTyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspVal | 80 |
| Db | 407 | GACACGGGTATACAGTATACGGCTCAAAATTCATACAGTGTCTGAAGGGTGGGACGTA | 466 |
| Qy | 81 | ValIleIleThrAlaGlyIleThrLysIleProGlyLysSerAspLysGluTyrSerArg | 100 |
| Db | 467 | GTAATATAACAGCAGCGGATAACAAAGATACCCGGAAGAGCGATAAAGATGTCCTAGA | 526 |
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| Db | 527 | ATGGATCTATTACCTGTAATATAAAGATAATAGGAGGTCGTCGACGAATTAATCT | 586 |
| Qy | 121 | TyrCysProAsnAlaPheValIleAsnIleThrAsnProLeuAspValMetValAlaAla | 140 |
| Db | 587 | TACTGTCTTAATGATTGTTATTAATATAACAAATCTCTTAGATGTGATGGTGTGCT | 646 |
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| Db | 647 | CTTCAAGAGTCATCAGGACTACCTCATAGAAATCTGCCGTATGCGTGGGATGCTTGAT | 706 |
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| Qy | 201 | AsnGlyIleProLeuSerGluPheValLysLysGlyTyrIleLysGlnGluValAsp | 220 |

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| Db | 827 | AAACGGCATCCCGCTTCTGAGTTGTTTAAAGAGGCGTCGATCAACGACGAAGAAGTAGAT | 886 |
| Qy | 221 | AspIleValGlnLysThrLysValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGly | 240 |
| Db | 887 | GATATCGTTTCAAGAACCAAGTCGCTCGAGAGAGATCGTACCGCTATTAGGACAGGC | 946 |
| Qy | 241 | SerAlaTyrTyrAlaProGlyValaSerAlaIleGlnMetAlaGluSerTyrLeuLysAsp | 260 |
| Db | 947 | TCTGCTTACTATGCTCCAGGGGCTTTCAGCTTATTCAGATGGCTGAGAGCTATCTAAAGAT | 1006 |
| Qy | 261 | ArgLysArgValMetValCysSerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHis | 280 |
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ORIGIN
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US-09-390-846-2 (1-330) x AY143389 (1-1411)

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Qy 61 AspThrGlyIleThrValTyrGlySerAsnSerTyrGluCysLeuLysGlyAlaAspVal 80
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RESULT 3
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 LOCUS Eimeria tenella lactate dehydrogenase (LDH) mRNA linear INV 18-MAY-2004
 ACCESSION AY143389
 VERSION AY143389.1 GI:25989638
 KEYWORDS
 SOURCE Eimeria tenella
 ORGANISM Eimeria tenella
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
 Eimeria.
 REFERENCE 1 (bases 1 to 1876)
 AUTHORS Schaap,D., Arts,G., Kroeze,J., Niessen,R., Roosmalen-Vos,S.V.,
 Spreuwerberg,K., Kuiper,C.M., Beek-Verhoeven,N.V.D., Kok,J.J.,
 Knegtel,R.M.A. and Vermeulen,A.N
 TITLE An Eimeria vaccine candidate appears to be lactate dehydrogenase;
 characterization and comparative analysis
 JOURNAL Parasitology 128 (6), 603-616 (2004)
 REFERENCE 2 (bases 1 to 1876)
 AUTHORS Schaap,D.C.
 TITLE Characterization and cloning of lactate dehydrogenase from three
 Eimeria species
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1876)
 AUTHORS Arts,G., Kroezen,H. and Schaap,D.C.
 TITLE Direct Submission
 JOURNAL Submitted (20-AUG-2002) Parasitology R&D, Intervet, Wim de
 Korversstraat, Boxmeer 5830AA, The Netherlands
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US-09-390-846-2 (1-330) x AY143389 (1-1876)

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RESULT 4
TGU23207
LOCUS
DEFINITION
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ACCESSION
U23207
VERSION
U23207.1
GT:975280
KEYWORDS
Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.

ORGANISM
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REFERENCE
1 (bases 269 to 909; 911 to 1249)
AUTHORS
Yang, S. and Parmley, S.F.
TITLE
A bradyzoite stage-specifically expressed gene of Toxoplasma gondii
encodes a polypeptide homologous to lactate dehydrogenase
Mol. Biochem. Parasitol. 73 (1-2), 291-294 (1995)
PUBMED
8577343
REFERENCE
2 (bases 1 to 2593)
AUTHORS
Parmley, S.F.
TITLE
Direct Submission
JOURNAL
Submitted (22-MAR-1995) Stephen F. Parmley, Immunology and
Infectious Diseases, Research Institute, Palo Alto Medical
Foundation, 860 Bryant Street, Palo Alto, CA 94301, USA
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Qy      289 GlyArgGlyValGluLysIleGluLeuGluIleThrAlaGlnGluArgGlnGlu 308
Db      1130 GGCGGTGGGGAATCGAGCAGGTATCGCACTGAGGTGACACATGAGGAACAAGAGTGT 1189
Qy      309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAlaIleAlaLeu 326
Db      1190 TTCAGGAATCAGTTGATGAGTGTGATGAATTGAATGAAGTTTAGCGGCGCTG 1243

RESULT 5
LOCUS   TGU35118 1822 bp mRNA linear INV 05-FEB-1997
DEFINITION Toxoplasma gondii lactate dehydrogenase mRNA, complete cds.
ACCESSION U35118
VERSION   U35118.1 GI:1695771
KEYWORDS
SOURCE    Toxoplasma gondii
          Toxoplasma gondii
          Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
          Sarcocystidae; Toxoplasma.
REFERENCE 1 (bases 1 to 1822)
          Yang, S. and Parmley, S.F.
          Toxoplasma gondii expresses two distinct lactate dehydrogenase
          homologous genes during its life cycle in intermediate hosts
          Gene 184 (1), 1-12 (1997)
JOURNAL   9016946
PUBMED
REFERENCE 2 (bases 1 to 1822)
          Parmley, S.F.
          Direct Submission
          Submitted (30-AUG-1995) Stephen F. Parmley, Immunology and
          Infectious Diseases, Research Institute, Palo Alto Medical
          Foundation, 860 Bryant Street, Palo Alto, CA 94301, USA
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1134..1822
3'UTR
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Score: 1041.50 Matches: 194
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Best Local Similarity: 60.4% Mismatches: 71
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Qy      29 SerLeuArgGlnLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
Db      228 GCTCTCGTGAGTCTGCTGACGCTCTCTAGATGTTGTCAAGGTATGCCGAGGT 287
Qy      49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
Db      288 AAGGCTCTTACCTGAGCCATGTGACCTCGTGGTGCACACCAACGTTTCGTCGGTGT 347
Qy      69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleThrAlaGlyIle 87
Db      348 GAGTACTCTTACGAGGCGCGCTCACCGGTGCGGACTGCTGTATCTGTTACGCGCGTCTG 407
Qy      88 ThrIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsn 107
Db      408 ACCAAGTGGCGGCAAGCCGAGCTCGAGTGAGCGCAACGATCTGCTCCCGTTCAAC 467
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Qy      128 IleAsnIleThrAsnProLeuAspValMetValAlaLeuGlnGluSerSerGlyLeu 147
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Qy      148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
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Qy      168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
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Qy      208 PheValLysLysGlyTrpIleLysGlnGluValAspAspIleValGlnLysThrLys 227
Db      768 TTCATCAAGGACGCGGTAGTCACGAGAGAGAGCTCGAGGAGATCGTGTGAGCACACAAA 827
Qy      228 ValAlaGlyGlyLysIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGly 247
Db      828 GTGCTGGCGGCGAGATCGTCCGCTTCTCTGCGGCGAGGTTCCTGCTGCTGCTGCTGCTG 887
Qy      248 AlaSerAlaIleGlnMetAlaGluSerTyrTyrLeuLysAspArgLysArgValMetValCys 267

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 Db 948 AGTGTGCTGCAACGAGAGTACGGCTTGAAGACATGTTCTATGTTCTCCCGCGCTC 1007
 Qy 288 IleGlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnGluArgGln 307
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 Qy 328 Ala 328
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 DEFINITION Sequence 311 from patent US 6514694.
 ACCESSION AR279170
 VERSION AR279170.1 GI:29713813
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 1785)
 AUTHORS Milhausen,M.J.
 TITLE Methods for the detection of encysted parasites
 JOURNAL Patent: US 6514694-A 311 04-FEB-2003;
 Heaska Corporation; Fort Collins, CO
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 Location/Qualifiers
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 Pred. No.: 4.95e-78 Length: 1785
 Score: 1034.50 Matches: 193
 Percent Similarity: 77.3% Conservative: 55
 Best Local Similarity: 60.1% Mismatches: 72
 Query Match: 61.3% Indels: 1
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 DB: 1
 US-09-390-846-2 (1-330) x AR279170 (1-1785)
 Qy 9 ArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeuCys 28
 Db 109 AGAAGAGGTGGCCATGATGGCTCTGGCATGATTGGTGGCACTATGGGCTACCTGTGC 168
 Qy 29 SerLeuArgGluLeuGlyAspValValPheAspValValProAsnMetProMetGly 48
 Db 169 GCTCTCGTGAGTCGCTGAGCTGCTCTACGATGTTCTCAAGTATGCCCGAGGT 228
 Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
 Db 229 AAGGCTTTCAGCTGAGCCATGTGACCTCGGTGTGCACCAACAGTTTCGGTCCGTGCT 288
 Qy 69 SerAsnSerTyrGlu---CysLeuLysGlyAlaAspValValIleThrAlaGlyIle 87
 Db 289 GAGTACTCTTACGAGGCGCGCTCACCGTGGCGACTGCGTTATCGTTACCGCGGCTG 348
 Qy 88 ThrLysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuLeuProValAsn 107
 Db 349 ACCAAGTGGCGGCAAGCCGACTCCGAGTGGAGCGCAACGATCTGCTCCCGTTCAAC 408
 Qy 108 IleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheVal 127
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Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeu 147
 Db 469 ATCGTGTCCACCAACCCGCTGAGTGCATGGTCAAGGTCAATGTCGAGGCTCTGGCGTC 528
 Qy 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet 167
 Db 529 CCGACCAACATGATCTGCGGTATGGCTCGCATGCTGACTCTGGTCTGCTCCGCCGATAC 588
 Qy 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
 Db 589 GTCGCCGAGCGGCTGTCTCTCTCCCGCAGCTCCAGGCCACCGTCAATCGGCACACAC 648
 Qy 188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu 207
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 Db 709 TTTCATCAGGACGGCGTAGTACGGAGAAGAGCTCGAGGAGATCGCTGAGCACACCAA 768
 Qy 228 ValAlaGlyGlyGluIleValArgLeuGlyGlnGlySerAlaTyrTyrAlaProGly 247
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 Qy 248 AlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCys 267
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 Qy 268 SerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysVal 287
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 Qy 288 IleGlyGlyArgGlyValGluLysIleIleGluLeuGluLeuThrAlaGlnArgGln 307
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 Db 1069 GCG 1071
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 DEFINITION Sequence 313 from patent US 6514694.
 ACCESSION AR279171
 VERSION AR279171.1 GI:29713814
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 1785)
 AUTHORS Milhausen,M.J.
 TITLE Methods for the detection of encysted parasites
 JOURNAL Patent: US 6514694-A 313 04-FEB-2003;
 Heaska Corporation; Fort Collins, CO
 FEATURES
 Location/Qualifiers
 source 1..1785
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 ORIGIN
 Alignment Scores:
 Pred. No.: 4.95e-78 Length: 1785
 Score: 1034.50 Matches: 193
 Percent Similarity: 77.3% Conservative: 55
 Best Local Similarity: 60.1% Mismatches: 72
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US-09-390-846-2 (1-330) x AR279171 (1-1785)

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 Qy 108 IleLysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheVal 127
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 Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeu 147
 Db 469 ATCGTGTGTACCAACCCGCTGACATGTCATGTCGATGTCGAGGCTCTGCGGTC 528
 Qy 148 ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgArgMet 167
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 Qy 168 IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis 187
 Db 589 GTCCCGCAGCGCTGTCTGTCTCTCCCGGACGCTCAGGCCACCGTCATCGGCACACAC 648
 Qy 188 GlyAspHisMetValProLeuSerArgTyrAlaThrValAlaGlyIleProLeuSerGlu 207
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 Qy 208 PheValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLys 227
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 Qy 228 ValAlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGly 247
 Db 769 GTGTCTGGCGGAGATCGCTCGCTTCTCGCGCAGGGTTCGCTTACTAGCCCCCGCC 828
 Qy 248 AlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCys 267
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 Qy 268 SerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysVal 287
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 Qy 328 Ala 328
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RESULT 8
 AY650028
 LOCUS

951 bp mRNA linear INV 07-JUL-2004

DEFINITION

Toxoplasma gondii strain RH malate dehydrogenase mRNA, complete cds.

ACCESSION AY650028.1 GI:49617504

VERSION

KEYWORDS

SOURCE

ORGANISM

Toxoplasma gondii

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocystidae; Toxoplasma.

1 (bases 1 to 951)

Shen, C., Zhan, X., He, A. and Li, Z.

Direct Submission

Submitted (10-JUN-2004) Department of Parasitology, Zhongshan

Medical College, Sun Yat-Sen University, Guangzhou, Guangdong

510089, China

FEATURES

Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 1,91e-67 Length: 951
 Score: 905.50 Matches: 173
 Percent Similarity: 73.0% Conservative: 57
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 DB: 2 Gaps: 1

US-09-390-846-2 (1-330) x AY650028 (1-951)

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Db 4 TCTCGAAGAAAATCGCCCTCATCGCGCGGCGCAACATCGCGCCACGCTTGCCTTCTC 63

Qy 28 CysSerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMet 47

Db 64 TCCGCTGTCAAGGAATCGCGGACGTCGTCTATGTTCCAGCTCGTCAGGACCTCCCGAA 123

Qy 48 GlyLysAlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrValTyr 67

Db 124 GGAATAATCGCTCGATCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 183

Qy 68 GlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleThrAlaGlyIle 87

Db 184 GGCTCGAACACTACAGCGTCTCAAGGATCGGATGTCATCATCGTCTGACGAGGGTG 243

Qy 88 ThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuProValAsn 107

Db 244 CCTCGGAGCCAGGT-----ATGCTCGCCGACGCTGCTGGCGATTAC 288

Qy 108 IleLysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheVal 127

Db 289 GCGAAAATCATGGCCAAAGTTGGAAGCCATCAAGCAGTACTGCCCCAACGCACTTCGTC 348

Qy 128 IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeu 147

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| Qy | 168 | IleAlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHis | 187 |
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| Qy | 188 | GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu | 207 |
| Db | 529 | GSAGACACCATGTGTGCCCTCCCTCGATTCCACCATGTGGGAGGCATCCCCCTCGCTGAG | 588 |
| Qy | 208 | PheValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLys | 227 |
| Db | 589 | CTGGTGAAGATGGGTATGATTTCTCAACAAGAGTGCAGATATCGTCCATGGGTGGCCAT | 648 |
| Qy | 228 | ValAlaGlyGlyLueValArgLeuLeuGlyGlnGlySerAlaTyrAlaProGly | 247 |
| Db | 649 | AATGGAGGTGGAGAAATCGTCTCATTCGTAAGACGGGCTCTGCTTCTTCGCTCCCGCG | 708 |
| Qy | 248 | AlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCys | 267 |
| Db | 709 | GCTCGGGCGCTCTGTATGGCGGAGGCGGTACTCTGAAGACCGCAAAACGCTGCTCCTGT | 768 |
| Qy | 268 | SerCysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysVal | 287 |
| Db | 769 | CGCGCTATTGTAACGAGAGTACGGTCTCAAGACATGATGTGGCGGTGCGCTGCGTG | 828 |
| Qy | 288 | IleGlyGlyArgGlyValGlyLysIleIleGlyLeuLeuLeuThrAlaGlnArgGln | 307 |
| Db | 829 | ATCGCGCGGCGCGTCGAGAAGATTGTCGAATTGACCTTGACGCTGAGGAGAAAG | 888 |
| Qy | 308 | GluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAla | 322 |
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| VERSION | AY972525.1 | GI:62465590 | |
| KEYWORDS | toxoplasma gondii | | |
| SOURCE | toxoplasma gondii | | |
| ORGANISM | Rukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma. | | |
| REFERENCE | 1 (bases 1 to 951) | | |
| AUTHORS | Chan, M. and Sim, T. S. | | |
| TITLE | Functional characterization of an alternative [lactate dehydrogenase-like] malate dehydrogenase in Plasmodium falciparum | | |
| JOURNAL | Parasitol. Res. 92 (1), 43-47 (2004) | | |
| PUBMED | 14598170 | | |
| REFERENCE | 2 (bases 1 to 951) | | |
| AUTHORS | Shen, C., Zhan, X., Zheng, X., Zheng, B., He, A., Li, Z. and Zheng, H. | | |
| TITLE | Cloning and characterization of the malate dehydrogenase gene from Toxoplasma gondii | | |
| JOURNAL | Zhongguo Ren Shou Gong Huan Bing Za Zhi 21 (2005) In press | | |
| REFERENCE | 3 (bases 1 to 951) | | |
| AUTHORS | Shen, C., Zhan, X., Zheng, X., Zheng, B., He, A., Li, Z. and Zheng, H. | | |
| TITLE | Direct Submision | | |
| JOURNAL | Submitted (23-MAR-2005) Department of Parasitology, Zhongshan Medical College, Sun Yat-sen University, Guangzhou, Guangdong 510089, China | | |
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| | LNVSVDLHALVMGGHDTMPLPRFTTVGGIPLPELVKMGMSIQOEVDDIVORTNG | | |
| | GGEIVSLLTGSFAFPAPAAAGVLMAEAYLKDKRVLPCAAYLNGEYGVKDMYGVPCV | | |
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| ORIGIN | | | |
| Alignment Scores: | | | |
| Prod. No.: | 1..91e-67 | Length: | 951 |
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| Best Local Similarity: | 54.9% | Mismatches: | 80 |
| Query Match: | 53.6% | Indels: | 5 |
| DB: | 2 | Gaps: | 1 |
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| Qy | 8 | ThrArgProLysIleAlaMetValGlySerGlyMetIleGlyThrMetAlaPheLeu | 27 |
| Db | 4 | TCTCGAAGAAAAATCGGCCTCATCGCGCGGCAACATCGCGCCACGCTTGCCTTCTC | 63 |
| Qy | 28 | CysSerLeuArgGluLeuGlyAspValValLeuPheAspValValProMet | 47 |
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| Qy | 48 | GlyLysAlaMetAspIleSerHisAsnSerValValAspThrGlyIleThrValTyr | 67 |
| Db | 124 | GGAAAAATGCTCGATCTGTACCGATTGATCTCGATCTCTGGAGTTGACGTTCTCGAG | 193 |
| Qy | 68 | GlySerAsnSerTyrGluCysLeuLysGlyAlaAspValValIleThrAlaGlyIle | 87 |
| Db | 184 | GGCTCGAAGCACTACACGCTCTCAAGGATCGGATGTCATCATCATCTGCTACTGCA | 243 |
| Qy | 88 | ThrLysIleProGlyLysSerAspLysGluTyrSerArgMetAspLeuProValAsn | 107 |
| Db | 244 | CCTCGAAGCAAGT-----ATGCTCTCGGACGACCTGCTGGCGATTAAAC | 288 |
| Qy | 108 | IleLysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheVal | 127 |
| Db | 289 | CGAAATCATGGCCCAAGTTGGAGAGCCATCAACAGTACTGCCCCAACGATTCGTC | 348 |
| Qy | 128 | IleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSerGlyLeu | 147 |
| Db | 349 | ATTGTCATCAGCAATCCATCGATGTGATGGTGTACATCTCTCGCGAAATAATCGGCTT | 408 |
| Qy | 148 | ProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMet | 167 |
| Db | 409 | CCTCCCAACAAAGTTTGGCGCATGGCGCGCTCTCGACTCAGCTCGGCTTCGACGTTT | 468 |
| Qy | 168 | IleAlaAspLysLeuValSerProArgAspValGlnGlyMetValIleGlyValHis | 187 |
| Db | 469 | CTCTCGAGCGCTCTCAACGCTCTCCGTCGATGATCATCACGCCCTCGTATGGGTGGCCAT | 528 |
| Qy | 188 | GlyAspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGlu | 207 |
| Db | 529 | GGAGACACCATGGTGGCCCTCCCTCGATTCACCACTGTGGGAGGCATCCCTCGCTGAG | 588 |
| Qy | 208 | PheValLysLysGlyTyrIleLysGlnGluValAspIleValGlnLysThrLys | 227 |
| Db | 589 | CTGGTGAAGATGGGTATGATTTCTCAACAAGAGTGCAGATATCGTCCACACGCACTCGC | 648 |
| Qy | 228 | ValAlaGlyGlyLueValArgLeuLeuGlyGlnGlySerAlaTyrAlaProGly | 247 |
| Db | 649 | AATGGAGGTGGAGAAATCGTCTCATTCGTAAGACGGGCTCTGCTTCTTCGCTCCCGCG | 708 |
| Qy | 248 | AlaSerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCys | 267 |


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Qy      288  IleGlyGlyArgGlyValGluLysAlaIleGluLeuGluLeuThrAlaGlnGluArgGln 307
Db      829  ATCGCGCGCGCGCGTCAAGAGATTGTCAATTGGACTTGACCGCTTGAGGAGAGAAG 888
Qy      308  GluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAla 322
Db      889  ATGTTGAGCGCTCGTTGAAGTGTGAAGCGCTTCTCGCGCT 933

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DEFINITION Rhizobium leguminosarum mdh gene and partial succ gene and partial
            gene encoding putative ATPase.
ACCESSION AJ002750
VERSION    AJ002750.1 GI:2624393
KEYWORDS   ATPase; malate dehydrogenase; mdh gene; succ gene; succinyl-CoA
            synthetase beta-subunit.
SOURCE     Rhizobium leguminosarum
ORGANISM   Rhizobium leguminosarum
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
REFERENCE  1
AUTHORS    Walshaw,D.L., Wilkinson,A., Mundy,M., Smith,M. and Poole,P.S.
TITLE      Regulation of the TCA cycle and the general amino acid permease by
            overflow metabolism in Rhizobium leguminosarum
JOURNAL    Microbiology (Reading, Engl.) 143 (Pt 7), 2209-2221 (1997)
PUBMED     9245810
REFERENCE  2 (bases 1 to 1839)
AUTHORS    Poole,P.S., Allaway,D. and Smith,M.
TITLE      Regulation of the mdh-suc operon of Rhizobium leguminosarum
JOURNAL    Unpublished
REFERENCE  3 (bases 1 to 1839)
AUTHORS    Poole,P.S.
TITLE      Direct Submission
JOURNAL    Submitted (12-NOV-1997) Poole P.S., Division of Microbiology,
            University of Reading, School of AMS University of Reading,
            Whiteknights, Reading, RG6 6AJ, UK
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Pred. No.:      9,96e-66      Length:      1839
Score:          889.50      Matches:      172
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US-09-390-846-2 (1-330) x RLAJ2750 (1-1839)

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Db      643  CTGACGGCGCCAGCGACTATTTCGGCATCGAAGGCGCTGACGTCTCATCTGTCACGCG 702
Qy      86  GlyIleThrLysIleProGlyLysSerAspLysGluTrpSerArgMetAspLeuLeuPro 105
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Qy      126  PheValIleAsnIleThrAsnProLeuAspValMetValAlaAlaLeuGlnGluSerSer 145
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Qy      146  GlyLeuProHisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArg 165
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 Qy 286 CysValIleGlyArgGlyValGlnLysIleLeuGluLeuGluLeuThraAlaGlnGlu 305
 Db 1288 ACCGTCATCGCGCGCGCGCTCGAGCGCATCATCGATCGATCTCAACAAGACCGAG 1347
 Qy 306 ArgGlnGluLeuGlnGlySerIleAspGluValLysGluMetGlnLysAla 322
 Db 1348 AAGGAAGCCTTCGACAAAGTCGTCGCGCGCTGCTCGGAGGCC 1398
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 LOCUS AB112429 1350 bp mRNA linear INV 08-JUN-2004
 DEFINITION Babesia bovis mRNA for L-lactate dehydrogenase, complete cds.
 ACCESSION AB112429
 VERSION AB112429.1 GI:31790621
 KEYWORDS
 SOURCE Babesia bovis
 ORGANISM Babesia bovis
 Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
 Babesia.
 REFERENCES
 1 Bork.S., Okamura, M., Boonchit, S., Hirata, H., Yokoyama, N. and Igarashi, I.
 Identification of Babesia bovis L-lactate dehydrogenase as a potential chemotherapeutic target against bovine babesiosis Mol. Biochem. Parasitol. 136, 165-172 (2004)
 2 (bases 1 to 1350)
 YOKOYAMA, N. and IGARASHI, I.
 Direct Submission
 Submitted (13-JUN-2003) Noaki Yokoyama, National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Inada-cho, Obihiro, Hokkaido 080-8555, Japan (E-mail: yokoyama@obihiro.ac.jp, Tel: 81-155-49-5649, Fax: 81-155-49-5643)
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Percent Similarity: 72.4% Conservative: 62
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 Query Match: 52.7% Indels: 0
 DB: 2 Gaps: 0
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 Qy 29 SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly 48
 Db 152 CAACTGAGGAACCTTGGCGATGTAGTACTCTTCGACATTGCACCAAAATGGGTGCTGCC 211
 Qy 49 LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyrGly 68
 Db 212 AAGGCTTTGGATATCATGCACGCAATGCCATCTACGATACCTCCCAAAATGTTATGGT 271
 Qy 69 SerAsnSerTyrCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr 88
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 Qy 89 LysIleProGlyLysSerAspLysGluTyrPheArgMetAspLeuLeuProValAsnIle 108
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 Qy 109 LysIleMetArgGluValGlyAlaAlaIleLysSerTyrCysProAsnAlaPheValIle 128
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 RESULT 12
 DQ060151

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| Qy | 9 | ArgProLysIleAlaMetValGlySerGlyMetIleGlyGlyThrMetAlaPheLeu | Cys 28 |
| Db | 10 | AAACCCAAAATTTGTGTCGTGGGTGGGCATGATCGGAGGCGTGATGGCCACGCTGATT | 69 |
| Qy | 29 | SerLeuArgGluLeuGlyAspValValLeuPheAspValValProAsnMetProMetGly | 48 |
| Db | 70 | GTGCAGAGAACCTGGGGGACGTAGTGATGTTTGACGTAGTGAAAAAATGCCCCCAAGGA | 121 |
| Qy | 49 | LysAlaMetAspIleSerHisAsnSerSerValValAspThrGlyIleThrValTyGly | 68 |
| Db | 130 | AAGGCACATAGATAGCTCTCACTCGAATGTGATGGCTTATTCCAATTCGAAGTGA | 181 |
| Qy | 69 | SerAsnSerTyGluCysLeuLysGlyAlaAspValValIleIleThrAlaGlyIleThr | 88 |
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BX897699_19 1900001 1931047
Continuation (20 of 20) of BX897699 from base 1900001 (BX897699 Bartonella henselae str)

Alignment Scores:

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Score: 880.50 Matches: 169
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DB: 1 Gaps: 1

US-09-390-846-2 (1-330) x BX897699_19 (1-31047)

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ACCESSION AE009456 AE008917
VERSION AE009456.1 GI:17982006
KEYWORDS
SOURCE
ORGANISM Brucella melitensis 16M
Brucella melitensis 16M
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
1 (bases 1 to 1111)
DelVecchio,V.G., Kapratl,V., Redkar,R.J., Patra,G., Mujer,C.,
Los,T., Ivanova,N., Anderson,I., Bhattacharyya,A., Lykidis,A.,
Reznik,G., Jablonski,L., Larsen,N., D'Souza,M., Bernal,A.,
Mazur,M., Goltzman,E., Selkov,E., Elzer,P.H., Hagius,S.,
O'Callaghan,D., Letesson,J.-J., Haselkorn,R., Kyripides,N. and
Overbeek,R.
The genome sequence of the facultative intracellular pathogen
Brucella melitensis
Proc. Natl. Acad. Sci. U.S.A. 99 (1), 443-448 (2002)
11756688
2 (bases 1 to 1111)
DelVecchio,V.G., Redkar,R.J., Patra,G. and Mujer,C.
Direct Submission
Submitted (13-NOV-2001) Institute of Molecular Biology and
Medicine, University of Scranton, Scranton, PA 18510, USA
3 (bases 1 to 1111)
Elzer,P.H. and Hagius,S.
Direct Submission
Submitted (13-NOV-2001) Department of Veterinary Science, LSU Ag
Center, 111 Dalrymple Building, Baton Rouge, LA 70803, USA
4 (bases 1 to 1111)
Kapratl,V., Los,T., Ivanova,N., Anderson,I., Bhattacharyya,A.,
Lykidis,A., Reznik,G., Jablonski,L., Larsen,N., D'Souza,M.,
Bernal,A., Mazur,M., Goltzman,E., Selkov,E., Haselkorn,R.,
Kyripides,N. and Overbeek,R.
Direct Submission
Submitted (13-NOV-2001) Integrated Genomics, Inc., 2201 W. Campbell
Park Drive, IL 60612, USA
5 (bases 1 to 1111)
Letesson,J.-J.
Direct Submission
Submitted (13-NOV-2001) Unite de Recherche en Biologie Moleculaire,
Laboratoire d'Immunologie et de Microbiologie, Universite of Namur,
61 rue de Bruxelles, Namur 5000, Belgium
6 (bases 1 to 1111)
O'Callaghan,D.
Direct Submission
Submitted (13-NOV-2001) Faculte de Medecine, INSERM U431, Avenue
Kennedy, Nimes 30900, France
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| Alignment Scores: Pred. No.: 1,21e-63 Length: 11111 Score: 876.50 Matches: 174 Percent Similarity: 70.7% Conservatives: 53 Best Local Similarity: 54.2% Mismatches: 89 Query Match: 51.9% Indels: 5 DB: 1 Gaps: 1 | | |


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Qy 109 LysIleMetArgGluValGlyAlaIleLysSerTyrCysProAsnAlaPheValIle 128
Db 292 AAGGTCATGGAAAGGTCGCGCCGCGCATCAAGAAATAGCTCCGAAGCCTTCGTGATC 351
Qy 129 AsnIleThrAsnProLeuAspValMetValAlaIleLeuGlnGluSerSerGlyLeuPro 148
Db 352 TGCATCACCAACCCGCTGACCCATGGTCTGGGCGCTGCAGAAAGTTCTTCGGCCCTGCCG 411
Qy 149 HisHisArgIleCysGlyMetAlaGlyMetLeuAspSerSerArgPheArgMetIle 168
Db 412 AAGAACAAAGGTCGTCGGCATGCGCGCGTCTCGACTCTTCGGCTTCGGCTCTTCCTC 471
Qy 169 AlaAspLysLeuGluValSerProArgAspValGlnGlyMetValIleGlyValHisGly 188
Db 472 GCCGAAGAGTTCAACGCTCTGTCAAGACATCACCGCTTTCGTCTCGGGCGCATGGC 531
Qy 189 AspHisMetValProLeuSerArgTyrAlaThrValAsnGlyIleProLeuSerGluPhe 208
Db 532 GACACCATGGTCCGCTCGCGGTATTTCGACGGTTGCCGGCATCCCGTGCAGACCTG 591
Qy 209 ValLysLysGlyTyrIleLysGlnGluValAspAspIleValGlnLysThrLysVal 228
Db 592 ATCCAGATGGTTGCACCACCAAGAAAGCTCGACCATTCATTCAGCGCACCCGTGAC 651
Qy 229 AlaGlyGlyGluIleValArgLeuLeuGlyGlnGlySerAlaTyrTyrAlaProGlyAla 248
Db 652 GCGCGCGCGAGATCGTCGGCTTGCTCAAGACCGCTCGGCTATTATGCGCGCGCGCC 711
Qy 249 SerAlaIleGlnMetAlaGluSerTyrLeuLysAspArgLysArgValMetValCysSer 268
Db 712 TCGCGCATCGAAATGCCGAAGCCTATCTCAAGGACAAAGACCGCGTCTGCCCTCGCGCC 771
Qy 269 CysTyrLeuGlnGlyGlnTyrGlyValGlnAsnHisTyrLeuGlyValProCysValIle 288
Db 772 GCTCATCTCTCCGGCCAGTATGGCGTCAAGGACATGTATGTGGCGTCCGCCACCGTGATC 831
Qy 289 GlyGlyArgGlyValGlyLysIleIleGluLeuGluLeuThrAlaGlnGluArgGlnGlu 308
Db 832 GGTGCCGCGCGCATCGAGCGCATCATCGAGATCGACCTCAACAAGGGCGGAGAGGAGCC 891
Qy 309 LeuGlnGlySerIleAspGluValLysGluMetGlnLysAla 322
Db 892 TTCGACAAAGTCGGTTGCGCGCGCTCGCCGCGCTTTCGGAAGCC 933
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Job time : 4623 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 19:41:36 ; Search time 67 Seconds
(without alignments)
2057.965 Million cell updates/sec

Title: US-09-390-846-2
Perfect score: 1688
Sequence: 1 MAVFKNTRPKIAMVSGMI.....GSIDEVKEMKATAALDASK 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------------|
| 1 | 880.5 | 52.2 | 320 | 4 | US-10-369-493-17838, A |
| 2 | 873.5 | 51.7 | 319 | 4 | US-10-369-493-11441, A |
| 3 | 873.5 | 51.7 | 320 | 4 | US-10-369-493-14499, A |
| 4 | 873.5 | 51.7 | 320 | 4 | US-10-369-493-14874, A |
| 5 | 862.5 | 51.1 | 311 | 4 | US-10-369-493-20748, A |
| 6 | 862.5 | 51.1 | 322 | 4 | US-10-369-493-12060, A |
| 7 | 850.5 | 50.4 | 320 | 4 | US-10-369-493-17079, A |
| 8 | 848.5 | 50.3 | 320 | 4 | US-10-369-493-8013, A |
| 9 | 847.5 | 50.2 | 320 | 4 | US-10-369-493-10523, A |
| 10 | 740 | 43.8 | 312 | 4 | US-10-369-493-23237, A |
| 11 | 709 | 42.0 | 314 | 4 | US-10-369-493-17395, A |
| 12 | 697 | 41.3 | 312 | 4 | US-10-369-493-16518, A |
| 13 | 689 | 40.8 | 285 | 4 | US-10-369-493-19127, A |
| 14 | 672 | 39.8 | 309 | 4 | US-10-369-493-9045, A |
| 15 | 669.5 | 39.7 | 319 | 4 | US-10-369-493-13585, A |
| 16 | 652.5 | 38.7 | 304 | 4 | US-10-369-493-10401, A |
| 17 | 649.5 | 38.5 | 325 | 4 | US-10-369-493-18220, A |
| 18 | 641 | 38.0 | 325 | 4 | US-10-724-972A-7257, A |
| 19 | 635 | 37.6 | 304 | 4 | US-10-369-493-11172, A |
| 20 | 635 | 37.6 | 317 | 4 | US-10-369-493-19850, A |
| 21 | 634 | 37.6 | 324 | 4 | US-10-369-493-2822, A |
| 22 | 628 | 37.2 | 299 | 4 | US-10-369-493-9764, A |
| 23 | 626.5 | 37.1 | 305 | 4 | US-10-369-493-10967, A |
| 24 | 625.5 | 37.1 | 309 | 4 | US-10-369-493-18858, A |
| 25 | 605.5 | 35.9 | 335 | 4 | US-10-369-493-138, A |
| 26 | 569 | 33.7 | 334 | 4 | US-10-369-493-125, A |
| 27 | 560.5 | 33.2 | 313 | 4 | US-10-369-493-22856, A |

| | | | | | | |
|----|-------|------|-----|---|---------------------|-------------------|
| 28 | 529 | 31.3 | 197 | 4 | US-10-369-493-14326 | Sequence 14326, A |
| 29 | 478 | 28.3 | 314 | 4 | US-10-369-493-18330 | Sequence 18330, A |
| 30 | 462 | 27.4 | 312 | 4 | US-10-369-493-16679 | Sequence 16679, A |
| 31 | 460 | 27.3 | 321 | 4 | US-10-369-493-23073 | Sequence 23073, A |
| 32 | 458 | 27.1 | 312 | 4 | US-10-369-493-16703 | Sequence 16703, A |
| 33 | 455 | 27.0 | 318 | 4 | US-10-154-460-46 | Sequence 46, Appl |
| 34 | 439.5 | 26.0 | 319 | 4 | US-10-369-493-3069 | Sequence 3069, Ap |
| 35 | 439 | 26.0 | 312 | 4 | US-10-369-493-16478 | Sequence 16478, A |
| 36 | 436 | 25.8 | 319 | 3 | US-09-971-361-3 | Sequence 3, Appl1 |
| 37 | 436 | 25.8 | 319 | 3 | US-09-971-361-9 | Sequence 9, Appl1 |
| 38 | 436 | 25.8 | 319 | 6 | US-11-108-870-3 | Sequence 3, Appl1 |
| 39 | 436 | 25.8 | 319 | 6 | US-11-108-870-9 | Sequence 9, Appl1 |
| 40 | 425 | 25.2 | 318 | 4 | US-10-369-493-3022 | Sequence 3022, Ap |
| 41 | 422 | 25.0 | 308 | 4 | US-10-369-493-3200 | Sequence 3200, Ap |
| 42 | 418.5 | 24.8 | 323 | 5 | US-10-873-467-76 | Sequence 76, Appl |
| 43 | 411.5 | 24.4 | 310 | 4 | US-10-369-493-17474 | Sequence 17474, A |
| 44 | 408 | 24.2 | 332 | 4 | US-10-170-385-223 | Sequence 223, App |
| 45 | 408 | 24.2 | 332 | 5 | US-10-873-595-3 | Sequence 3, Appl1 |

ALIGNMENTS

RESULT 1

US-10-369-493-17838
; Sequence 17838, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17838
; LENGTH: 320
; TYPE: PRT
; ORGANISM: SPHINGOMONAS
US-10-369-493-17838

| | | | | | | | |
|-----------------------|-------|---|-------|------------|----|--------|-----|
| Query Match | 52.2% | Score | 880.5 | DB | 4 | Length | 320 |
| Best Local Similarity | 53.9% | Pred. No. | 2e-79 | | | | |
| Matches | 173 | Conservative | 54 | Mismatches | 89 | Indels | 5 |
| Gaps | 1 | | | | | | |
| Qy | 9 | RPKIAMVSGMIGTMAFLCSLRELGDVVLFDVVPNNMPGKAMDISHNSVVDITGVYG | 68 | | | | |
| Db | 3 | RKIALIGSGMIGTMAFLCSLRELGDVVLFDVVPNNMPGKAMDISHNSVVDITGVYG | 62 | | | | |
| Qy | 69 | SNSYECLGADVVIIITAGITKIPKSDKEWSDMLLPVNIKIMREVGAAIKSYCPNAPVI | 128 | | | | |
| Db | 63 | ANSYEDIAGDVCIIVTAGIPRKEG-----MSRDDLLKTNLGVKAVGEGIAAHAPDAFVI | 117 | | | | |
| Qy | 129 | NTNPLDVMVAIQESSGLPHHRCIMAGMDSRFRMIADKLEIVSPRVDQGVIGVHG | 188 | | | | |
| Db | 118 | CITNPLDVMVAIQESSGLPHHRCIMAGMDSRFRMIADKLEIVSPRVDQGVIGVHG | 177 | | | | |
| Qy | 189 | DHMPVLSRYATVNGIPLSEFVKKGWIKQREVDVIVOKTVAGGEIVRLGQGSAYVAPGA | 248 | | | | |
| Db | 178 | DTNPVIEYSTVAGIVPDLIRKMGWSTQERIDAIVARTSRGGGEIVALLKTGSAYVAPAT | 237 | | | | |
| Qy | 249 | SATQMAESYLKDKRKMVGVSCVQQGVQVNHVLPVCPVIGGVRGVEKIIELELTAQERQE | 308 | | | | |
| Db | 238 | SATQMAESYLKDKRKMVGVSCVQQGVQVNHVLPVCPVIGGVRGVEKIIELELTAQERQE | 297 | | | | |
| Qy | 309 | LOGSIDEVKEMOKATAALDAS | 329 | | | | |

Db 298 FDVSDAVKELVAACKSIDAS 318

RESULT 2

US-10-369-493-11441

Sequence 11441, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 11441

LENGTH: 319

TYPE: PRT

ORGANISM: Agrobacterium tumefaciens

US-10-369-493-11441

Query Match 51.7%; Score 873.5; DB 4; Length 319;

Best Local Similarity 53.2%; Pred. No. 1e-78;

Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSRLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDGTGTVYG 68

Db 3 RKXIALIGSGMIGTTLAHLASLKELGDIVLFDIADGIPQKGKGLDIAQSGVEGFNAKLSG 62

Qy 69 SNSYECLKGADVVIITAGITKIPGKSKDESRMDLLPVNIKIMREVGAAIKSCPNAFVI 128

Db 63 ASDYAAIEGADVCIIVTAGVARKPG-----MSRDDLGLINLKVMEQVAGIKKYAPNAFVI 117

Qy 129 NITNPLDVMVAALQESSGLPHHRICMGAGMLDSSRFRMIADKLEVS PRDVGQWVG 188

Db 118 CITNPLDAMVWALQKPSGLPKNKVVMAGVLD SARFLPLAEEFNVSQDVTAFVLGGHG 177

Qy 189 DHMVPLSRYATVNGIPLSEFVKKGWIKOEVEDDIVQKTKVAGGEIVRLLGQGSAYYAPGA 248

Db 178 DTWVPLARYSTVGGVPLTDLVKMGWLTAELEQI IQRTRDGGAEIVGLLKTGSAYYAPAA 237

Qy 249 SAIQMAESYLKDRKRVNVCSCYLOGQYGVQNHVLPVCPVIGRGVKEIIIELELTAQEROE 308

Db 238 SAIEMAESYLKDKRVLPAAHLSGGYGVDDMVYGVPTIIGAGGIERVIEILNKEEEAA 297

Qy 309 LQGSIDEVKEMQKA 322

Db 298 FOKSVGAVAGLCEA 311

RESULT 3

US-10-369-493-114489

Sequence 11489, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 11489

LENGTH: 320

TYPE: PRT

ORGANISM: Agrobacterium tumefaciens

US-10-369-493-11489

Query Match 51.7%; Score 873.5; DB 4; Length 320;

Best Local Similarity 53.2%; Pred. No. 1e-78;

Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSRLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDGTGTVYG 68

Db 3 RKXIALIGSGMIGTTLAHLASLKELGDIVLFDIADGIPQKGKGLDIAQSGVEGFNAKLSG 62

Qy 69 SNSYECLKGADVVIITAGITKIPGKSKDESRMDLLPVNIKIMREVGAAIKSCPNAFVI 128

Db 63 ASDYAAIEGADVCIIVTAGVARKPG-----MSRDDLGLINLKVMEQVAGIKKYAPNAFVI 117

Qy 129 NITNPLDVMVAALQESSGLPHHRICMGAGMLDSSRFRMIADKLEVS PRDVGQWVG 188

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14489

LENGTH: 320

TYPE: PRT

ORGANISM: Agrobacterium tumefaciens

US-10-369-493-14489

Query Match 51.7%; Score 873.5; DB 4; Length 320;

Best Local Similarity 53.2%; Pred. No. 1e-78;

Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSRLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDGTGTVYG 68

Db 3 RKXIALIGSGMIGTTLAHLASLKELGDIVLFDIADGIPQKGKGLDIAQSGVEGFNAKLSG 62

Qy 69 SNSYECLKGADVVIITAGITKIPGKSKDESRMDLLPVNIKIMREVGAAIKSCPNAFVI 128

Db 63 ASDYAAIEGADVCIIVTAGVARKPG-----MSRDDLGLINLKVMEQVAGIKKYAPNAFVI 117

Qy 129 NITNPLDVMVAALQESSGLPHHRICMGAGMLDSSRFRMIADKLEVS PRDVGQWVG 188

Db 118 CITNPLDAMVWALQKPSGLPKNKVVMAGVLD SARFLPLAEEFNVSQDVTAFVLGGHG 177

Qy 189 DHMVPLSRYATVNGIPLSEFVKKGWIKOEVEDDIVQKTKVAGGEIVRLLGQGSAYYAPGA 248

Db 178 DTWVPLARYSTVGGVPLTDLVKMGWLTAELEQI IQRTRDGGAEIVGLLKTGSAYYAPAA 237

Qy 249 SAIQMAESYLKDRKRVNVCSCYLOGQYGVQNHVLPVCPVIGRGVKEIIIELELTAQEROE 308

Db 238 SAIEMAESYLKDKRVLPAAHLSGGYGVDDMVYGVPTIIGAGGIERVIEILNKEEEAA 297

Qy 309 LQGSIDEVKEMQKA 322

Db 298 FOKSVGAVAGLCEA 311

RESULT 4

US-10-369-493-14874

Sequence 14874, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14874

LENGTH: 320

TYPE: PRT

ORGANISM: Agrobacterium tumefaciens

US-10-369-493-14874

Query Match 51.7%; Score 873.5; DB 4; Length 320;

Best Local Similarity 53.2%; Pred. No. 1e-78;

Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSRLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDGTGTVYG 68

Db 3 RKXIALIGSGMIGTTLAHLASLKELGDIVLFDIADGIPQKGKGLDIAQSGVEGFNAKLSG 62

Qy 69 SNSYECLKGADVVIITAGITKIPGKSKDESRMDLLPVNIKIMREVGAAIKSCPNAFVI 128

Db 63 ASDYAAIEGADVCIIVTAGVARKPG-----MSRDDLGLINLKVMEQVAGIKKYAPNAFVI 117

Qy 129 NITNPLDVMVAALQESSGLPHHRICMGAGMLDSSRFRMIADKLEVS PRDVGQWVG 188

Db 118 CTTNPLDAMWALQKFSGLPKNVKVGAGVLDLSARFLFLAEENFVNSVDVTAFLVGGH 177
Qy 189 DHMPLSRATVNGIPISFVKKGWIKOEVDVDDIVQKTKVAGGIVRLGQGSAYYAPGA 248
Db 178 DTWVPLARYSTVGGVPLTDLVKGWLTAELEQIQRTRDGGAEIVGLLTKGSAYYAPAA 237
Qy 249 SATMAESYLKDKRVMVCSYLOGQGVQNHVGLVPCVIGRGVKEKIELELTAQERQE 308
Db 238 SALEMAESYLKDKRVLPAHAHLGSGQGVDDMYGVPTIIGAGGIERVIELNKEEAA 297
Qy 309 LQGSIDEVKEMQKA 322
Db 298 FQKSVGAVGLCEA 311

RESULT 5

US-10-369-493-20748
; Sequence 20748, Application US/10369493
; Publication No. US20030233675A1

GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20748
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Rhodospseudomonas palustris
US-10-369-493-20748

Query Match 51.1%; Score 862.5; DB 4; Length 311;
Best Local Similarity 53.8%; Pred. No. 1.3e-77;
Matches 169; Conservative 59; Mismatches 81; Indels 5; Gaps 1;
Qy 9 RPKIAMVGSQMIGTMAFLCSLRELGDVVLFDVVPNNPMKAMDISHNSSVVDITGITYG 68
Db 3 RDXIALIGSGOIGTTLAHLVGLKELGDVVLFDIAEAGVPGKALDIAESSPVDGFDKLTG 62
Qy 69 SNSYECLKGADVVIITAGITKIPKSKDKEWSDMLLPVNIKIMREVGAAIKSYCPNAPVI 128
Db 63 ANSYEATEGARVVITVAGVPRKPG-----MSRDDLLSINLKVMEQVAGIKKYAPDAFVI 117
Qy 129 NITNPLDVMVAALQESSGLPHRRICGMAGMLDSRFRMIADKLEVSPRDVQGMVIGVHG 188
Db 118 CTTNPLDAMWALQKAGSLPAKVGAGVLDLSARFRFLADEBNFVNSVEDVTAFLVGGH 177
Qy 189 DHMPLSRATVNGIPISFVKKGWIKOEVDVDDIVQKTKVAGGIVRLGQGSAYYAPGA 248
Db 178 DTWVPLVKYSTVAGIPLPDLVKMGWTSQARLDELVDTRNGGAEIVNLLTKGSAYYAPAS 237
Qy 249 SATMAESYLKDKRVMVCSYLOGQGVQNHVGLVPCVIGRGVKEKIELELTAQERQE 308
Db 238 SALEMAESYLKDKRVPVAAHLNGEYGVKDMTVGVVPVWIGDKGVERIVEIELAGDKEA 297
Qy 309 LQGSIDEVKEMQKA 322
Db 298 FDRSVAAVQGLVEA 311

RESULT 6

US-10-369-493-12060
; Sequence 12060, Application US/10369493
; Publication No. US20030233675A1

GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12060
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-12060

Query Match 51.1%; Score 862; DB 4; Length 322;
Best Local Similarity 53.5%; Pred. No. 1.5e-77;
Matches 174; Conservative 56; Mismatches 87; Indels 8; Gaps 2;
Qy 9 RPKIAMVGSQMIGTMAFLCSLRELGDVVLFDVVPNNPMKAMDISHNSSVVDITGITYG 68
Db 3 RNKIALIGSGMIGTTLAHLVGLKELGDVVLFDIAEAGIPOQKGLDIAQSSPVDGFDKLTG 62
Qy 69 SNSYECLKGADVVIITAGITKIPKSKDKEWSDMLLPVNIKIMREVGAAIKSYCPNAPVI 128
Db 63 VNDYAGIEGADVCIITVAGVPRKEG-----MSRDDLLSINLKVMEQVAGIKKYAPKAPVI 117
Qy 129 NITNPLDVMVAALQESSGLPHRRICGMAGMLDSRFRMIADKLEVSPRDVQGMVIGVHG 188
Db 118 CTTNPLDAMWALQKFSGLPKTHVVGAGVLDLSARFRFLAEFKVSVEDVTAFLVGGH 177
Qy 189 DHMPLSRATVNGIPISFVKKGWIKOEVDVDDIVQKTKVAGGIVRLGQGSAYYAPGA 248
Db 178 DSMVPMIRYSTVSGIPLPDLVKMGWTSKBLDQIVQTRDGGAEIVGLLTKGSAYYAPAA 237
Qy 249 SATMAESYLKDKRVMVCSYLOGQGVQNHVGLVPCVIGRGVKEKIELELTAQERQE 308
Db 238 SALEMAESYLKDKRVLPCAHLGSGQGVKGTIVGVVPVWIGAGGVERIIEIDLNKSEQKM 297
Qy 309 LQGSIDEVKEMQKA-----IAALDASK 330
Db 298 FESSVATVQGLTEACVKIAPQLASK 322

RESULT 7

US-10-369-493-17079
; Sequence 17079, Application US/10369493
; Publication No. US20030233675A1

GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17079
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-17079

| | | |
|--|-----|--|
| Query Match | | 50.4%; Score 850.5; DB 4; Length 320; |
| Best Local Similarity | | 51.1%; Pred. No. 2.1e-76; |
| Matches | | 164; Conservative 60; Mismatches 92; Indels 5; Gaps 1; |
| Qy | 9 | RPKIAMVGSNGMGTMAFLCSLRELGDVVLFDVVPNPMKAMDISHNSVVDGTGTVYG 68 |
| Db | 3 | RAKIALIGAGMIGTGLAHIAAREBELGDVILFDIAEGTPOGKALDIAEASAVFGKDVALKG 62 |
| Qy | 69 | SNSYECLKGADVVITAGITIKPKSKDEWSDLLPVNIKIMREYGAATKSYCPNAFVI 128 |
| Db | 63 | ANSYEEATAGADVCLVTAGVRKPG-----MSRDDLGINLKVMKAVGEGIKAHAPNAFVI 117 |
| Qy | 129 | NITNPLDMVMAALQESSGLPHHRICGMAGMLDSSRFRMIADKLEVSPRDVGQMGVIGVHG 188 |
| Db | 118 | CITNPLDMVMAALQESSGLPKGVNAGVLDSEARFAYFLAEATGVSVEIDHAWTLGGHG 177 |
| Qy | 189 | DHMPVLSRYATVNGIPUSEFVKKGWIKQEBEVDIVQTKVAGGEIVRLLCQGSAYYAPGA 248 |
| Db | 178 | DTWVPLVRYSTVAGIPLDVLQWGLSQDLDAIVERTRKGGGEIVALLKTGSAFYAPAE 237 |
| Qy | 249 | SAIOMAESYLKDKRVMVSCYLOGOYGVQNHVLPVPCVIGRGVKEKIELELTAQERQE 308 |
| Db | 238 | SATAMATSYLKDKRVLPCATYITGQGLNDLYVGVPPVIGAGGAEKIVFETNDDEKAM 297 |
| Qy | 309 | LOGSIDEVKEMQKAIADSDAS 329 |
| Db | 298 | FAKSVESVKGLEACKAIDSS 318 |
| RESULT 8 | | |
| US-10-369-493-8013 | | |
| ; Sequence 8013, Application US/10369493 | | |
| ; Publication No. US20030233675A1 | | |
| ; GENERAL INFORMATION: | | |
| ; APPLICANT: Cao, Yongwei | | |
| ; APPLICANT: Hinkle, Gregory J. | | |
| ; APPLICANT: Slater, Steven C. | | |
| ; APPLICANT: Goldman, Barry S. | | |
| ; APPLICANT: Chen, Xianfeng | | |
| ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF | | |
| ; FILE REFERENCE: 38-10(52052)B | | |
| ; CURRENT APPLICATION NUMBER: US/10/369,493 | | |
| ; CURRENT FILING DATE: 2003-02-28 | | |
| ; PRIOR APPLICATION NUMBER: US 60/360,039 | | |
| ; PRIOR FILING DATE: 2002-02-21 | | |
| ; NUMBER OF SEQ ID NOS: 47374 | | |
| ; SEQ ID NO 8013 | | |
| ; LENGTH: 320 | | |
| ; TYPE: PRT | | |
| ; ORGANISM: Rhodobacter sphaeroides | | |
| US-10-369-493-8013 | | |
| Query Match | | 50.3%; Score 848.5; DB 4; Length 320; |
| Best Local Similarity | | 50.8%; Pred. No. 3.3e-76; |
| Matches | | 163; Conservative 64; Mismatches 89; Indels 5; Gaps 1; |
| Qy | 9 | RPKIAMVGSNGMGTMAFLCSLRELGDVVLFDVVPNPMKAMDISHNSVVDGTGTVYG 68 |
| Db | 3 | RPKIALIGAGMIGTGLAHIAAREBELGDVILFDIAEGTPOGKALDIAEASAVFGKDVALKG 62 |
| Qy | 69 | SNSYECLKGADVVITAGITIKPKSKDEWSDLLPVNIKIMREYGAATKSYCPNAFVI 128 |
| Db | 63 | ANSYEEATAGADVCLVTAGVRKPG-----MSRDDLGINLKVMKAVGEGIKAHAPNAFVI 117 |
| Qy | 129 | NITNPLDMVMAALQESSGLPHHRICGMAGMLDSSRFRMIADKLEVSPRDVGQMGVIGVHG 188 |
| Db | 118 | CITNPLDMVMAALQESSGLPKGVNAGVLDSEARFAYFLAEATGVSVEIDHAWTLGGHG 177 |
| Qy | 189 | DHMPVLSRYATVNGIPUSEFVKKGWIKQEBEVDIVQTKVAGGEIVRLLCQGSAYYAPGA 248 |
| Db | 178 | DTWVPLVRYSTVAGIPLDVLQWGLSQDLDAIVERTRKGGGEIVALLKTGSAFYAPAT 237 |
| Query Match | | 50.2%; Score 847.5; DB 4; Length 320; |
| Best Local Similarity | | 52.0%; Pred. No. 4.2e-76; |
| Matches | | 167; Conservative 61; Mismatches 88; Indels 5; Gaps 1; |
| Qy | 9 | RPKIAMVGSNGMGTMAFLCSLRELGDVVLFDVVPNPMKAMDISHNSVVDGTGTVYG 68 |
| Db | 3 | RKIALIGAGMIGTGLAHIAAREBELGDVILFDVVEGPOGKALDLSQCQGVFEGFDANIIG 62 |
| Qy | 69 | SNSYECLKGADVVITAGITIKPKSKDEWSDLLPVNIKIMREYGAATKSYCPNAFVI 128 |
| Db | 63 | TNDYKGIAGADVIITAGVARKPG-----MSRDDLGINLKVMKAVGEGIRDNAPDAFVI 117 |
| Qy | 129 | NITNPLDMVMAALQESSGLPHHRICGMAGMLDSSRFRMIADKLEVSPRDVGQMGVIGVHG 188 |
| Db | 118 | CITNPLDMVMAALQESSGLPKGVNAGVLDSEARFAYFLAEATGVSVEIDHAWTLGGHG 177 |
| Qy | 189 | DHMPVLSRYATVNGIPUSEFVKKGWIKQEBEVDIVQTKVAGGEIVRLLCQGSAYYAPGA 248 |
| Db | 178 | DTWVPLVRYSTVNGIPVPLDVLQWGLSQDLDAIVERTRKGGGEIVALLKTGSAFYAPAA 237 |
| Qy | 249 | SAIOMAESYLKDKRVMVSCYLOGOYGVQNHVLPVPCVIGRGVKEKIELELTAQERQE 308 |
| Db | 238 | SGIAMAELYNQKRLIPCAAYVDGEYGVNGLYVGVPLVILANGVEKVEKIELELDDRAKGN 297 |
| Qy | 309 | LOGSIDEVKEMQKAIADSDAS 329 |
| Db | 298 | LQVSDAVDAKLEACKGIDPS 318 |
| RESULT 10 | | |
| US-10-369-493-23237 | | |
| ; Sequence 23237, Application US/10369493 | | |
| ; Publication No. US20030233675A1 | | |
| ; GENERAL INFORMATION: | | |
| ; APPLICANT: Cao, Yongwei | | |
| ; APPLICANT: Hinkle, Gregory J. | | |
| ; APPLICANT: Slater, Steven C. | | |
| ; APPLICANT: Goldman, Barry S. | | |
| ; APPLICANT: Chen, Xianfeng | | |
| ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF | | |

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 23237

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Bacillus subtilis

; US-10-369-493-23237

Query Match 43.8%; Score 740; DB 4; Length 312;

Best Local Similarity 45.9%; Pred. No. 2.5e-65;

Matches 147; Conservative 63; Mismatches 98; Indels 12; Gaps 3;

Qy 7 NTRPKIAMVSGMIGGTMAFLCSRELGDVVLFDV--VPNMPGKAMDISHNSSVVDGTI 64

Db 3 NTRKVSIVGAGTGATTAFLIAQKELADVLDIPOLENPTKGKALDMLSESPVQGFDA 62

Qy 65 TVYGSNIEYELKGDADVITAGITKIPIKSDKEWSRMDLLPNNIKIMREYGAIAKSYCPN 124

Db 63 KITGTSNYEDTAGSDIVITAGIARKEG-----MSRDDLVSTNEKIMRSVTQEIYKYS PD 117

Qy 125 AFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDVQGMVI 184

Db 118 SIIVLTNPVDAMTYAYKESGFPKRVIGQSGVLDTARFRTFVAEELNSVKDVTGFLV 177

Qy 185 GVHGDHMPVLSRYATVNGIPLSEFVKKGWIKQEBVDIVOKTKVAGGEIVRLLGQGSAYY 244

Db 178 GGGDDMVPLVRSYAGGIPLETLPK-----ERIDAIVERTRKGGGEIVNLLGNGSAYY 232

Qy 245 AGASAIQMAESYLKDRKRVWVCSCYLQGGYGVQNHVYLPVPCVIGGRGVEKIIIELELTAQ 304

Db 233 APAASLTEMVEAILKQRRVLPPTIAYLEGEYGYEIVLPTVGGNGLEQIIELELTDY 292

Qy 305 EROELQGSIDEVKEKQAKA 324

Db 293 ERAQLNKSVESVKNVMKVL 312

RESULT 11

US-10-369-493-17395

; Sequence 17395, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 17395

; LENGTH: 314

; TYPE: PRT

; ORGANISM: Bacillus halodurans

; US-10-369-493-17395

Query Match 42.0%; Score 709; DB 4; Length 314;

Best Local Similarity 44.0%; Pred. No. 3.3e-62;

Matches 140; Conservative 67; Mismatches 97; Indels 14; Gaps 4;

Qy 9 RPKIAMVSGMIGGTMAFLCSRELGDVVLFDVVPNM---PMGKAMDISHNSSVVDGTIT 65

Db 5 RRVSVIGAGTGATTALMAVQAQKELGDVLD-IPQMEGPTKGKALDMLSESTPVQGV DNV 63

Qy 66 VYGSNIEYELKGDADVITAGITKIPIKSDKEWSRMDLLPNNIKIMREYGAIAKSYCPNA 125

Db 64 ITGTSYETKSDSDVVTAGIARKEG-----MSRDDLVSTNAGIMKAVTKEVVVKHSPNA 118

Qy 126 FVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDVQGMVIG 185

Db 119 YIIVLTNPADAMTYTYVYKESGFPKRVIGQSGVLDTARFRTFVAQELNLSVEDITGFVLG 178

Qy 186 VGHDMVPLSRYATVNGIPLSEFVKKGWIKQEBVDIVOKTKVAGGEIVRLLGQGSAYYA 245

Db 179 GHGDDMVPLIRYSYAGGIPLEKL-----LPOERIDAIVERTRKGGGEIVGLLNGSAYYA 233

Qy 246 PGASAIQMAESYLKDRKRVWVCSCYLQGGYGVQNHVYLPVPCVIGGRGVEKIIIELELTAQ 305

Db 234 PAASLAEVMAEAILKQRRVLPPTIAYLEGEYGYEIVVGPVTLGGDGIKIELELTDDE 293

Qy 306 ROELQGSIDEVKEKQAKI 323

Db 294 KATFAKSIESVRNMSAL 311

RESULT 12

US-10-369-493-16518

; Sequence 16518, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 16518

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

; US-10-369-493-16518

Query Match 41.3%; Score 697; DB 4; Length 312;

Best Local Similarity 43.5%; Pred. No. 5.2e-61;

Matches 138; Conservative 65; Mismatches 102; Indels 12; Gaps 3;

Qy 9 RPKIAMVSGMIGGTMAFLCSRELGDVVLFDV--VPNMPGKAMDISHNSSVVDGTITV 66

Db 5 RRVSVIGAGTGATTTFFLLAQKELADVLDIPOLENPTKGKALDMLSEASPVQGFDAI 64

Qy 67 YGSNIEYELKGDADVITAGITKIPIKSDKEWSRMDLLPNNIKIMREYGAIAKSYCPNAF 126

Db 65 IGTSYADTADSDVVTAGIARKEG-----MSRDDLVATNSKIMKSIITRDIKHSNAI 119

Qy 127 VINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDVQGMVIG 186

Db 120 IVVLTNPVDAMTYSVFKBAGFPKRVIGQSGVLDTARFRTFVAQELNLSVKDITGFVLGG 179

Qy 187 HGDHMPVLSRYATVNGIPLSEFVKKGWIKQEBVDIVOKTKVAGGEIVRLLGQGSAYYAP 246

Db 180 HGDDMVPLVRSYAGGIPLETLPK-----ERLEAIVERTRKGGGEIVGLLNGSAYYAP 234

Qy 247 GASAIQMAESYLKDRKRVWVCSCYLQGGYGVQNHVYLPVPCVIGGRGVEKIIIELELTAQ 306

Db 235 AASLWEMTEAILKQRRVLPPTIAYLEGEYGYSDLVGLVGPVILGGNGIEKIELELTADEK 294

Qy 307 ROELQGSIDEVKEKQAKI 323

Db 295 EALDRSVESVRNVMKVL 311

RESULT 13
US-10-369-493-19127
; Sequence 19127, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19127
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-10-369-493-19127

Query Match 40.8%; Score 689; DB 4; Length 285;
Best Local Similarity 47.1%; Pred. No. 2.9e-60;
Matches 139; Conservative 58; Mismatches 86; Indels 12; Gaps 3;
QY 9 RPKIAMVSGMIGTMAFLCSLRELGDVVLFDV--VPMMPMGKAMDISHNSVVDGTIV 66
Db 1 KKKIGLGGQIGGNLALLAVQSLGDVLYDIPAAEGLVKGKALDINQLAAVDGDCRV 60
QY 67 YGNSYECLKADVVITAGITKIPGSKDKWSRMDLLPVNIKIMREVGAIAKSYCPNAP 126
Db 61 KGTDDKWDVAGSDVIIITAGMPKPG-----MSREDLLEINLKIMTVDVAGNIKOHAPNAP 115
QY 127 VINITPLDVMAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDVGQMVIGV 186
Db 116 VINVNPDLDAVYLAALAEVSGFVKERVIGQAGVLDAAARTFTIAMEAGVSVEDVQAMLMGGHG 175
QY 187 HGHMPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGQGSAYYAP 246
Db 176 HGGDMPVLRHRTVGGVPLTELAK-----DKDLAIKRTREGPELVGLYKTSAYFGP 230
QY 247 GASAQMAESYLKDRKRVWVCYLOGQYGVQNHVLPVPCVIGRGVGEKIELEL 301
Db 231 AACAIAMAESFLQDRKRVLPAAALLEGQYGVQNHVLPVPCVIGRGVGEKIEHTVEL 285

RESULT 14
US-10-369-493-9045
; Sequence 9045, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9045
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus

US-10-369-493-9045

Query Match 39.8%; Score 672; DB 4; Length 309;
Best Local Similarity 43.8%; Pred. No. 1.7e-58;
Matches 141; Conservative 54; Mismatches 111; Indels 16; Gaps 3;
QY 9 RPKIAMVSGMIGTMAFLCSLRELGDVVLFDVPMMPMGKAMDISHNSVVDGTIVYG 68
Db 2 RKKISIIAGAFVGSITTAHMLAAKELGDIVLDFVEGVPOGKALDLYEASPIEGFDFVRVTG 61
QY 69 SNSYECLKADVVITAGITKIPGSKDKWSRMDLLPVNIKIMREVGAIAKSYCPNAPVI 128
Db 62 TNNYADTANSDIVVTSGAPRKP-----MSREDLIKVNADITRACISQAAPLSPNAVII 116
QY 129 NITNPLDVMAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDVGQMVIGVHG 188
Db 117 MYNNPLDAMTYLAALAEVSGFVKERVIGQAGVLDAAARTFTIAMEAGVSVEDVQAMLMGGHG 176
QY 189 DHMPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGQGSAYYAPGA 248
Db 177 DEWVPLPRESTISGIPVSEF-----IAPDLAQIVERTKGGGEIVNLLKTSAYYAPAA 231
QY 249 SAIQMAESYLKDRKRVWVCYLOGQYGVQNHVLPVPCVIGRGVGEKIELELTAQERQE 308
Db 232 ATAQMVAEAVLKDKRVMVAAYLTGQYGLNDIYFGVPVILGAGGVGEKIELELPLNEEMAL 291
QY 309 LOGSIDEVKEMQKATAALDASK 330
Db 292 LNASAKAVR-----ATLDTLK 307

RESULT 15
US-10-369-493-13585
; Sequence 13585, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13585
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Thermoplasma volcanium
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(319)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-13585

Query Match 39.7%; Score 669.5; DB 4; Length 319;
Best Local Similarity 42.9%; Pred. No. 3.1e-58;
Matches 137; Conservative 68; Mismatches 91; Indels 23; Gaps 5;
QY 9 RPKIAMVSGMIGTMAFLCSLRELGDVVLFDVPMMPMGKAMDISHNSVVD 61
Db 3 RKKISVIGAGNVGATVQAOLATKELGDVVLFDVVDGIGPEKALDIOEGAPHWGLDGVV- 61
QY 62 TGITVYGSNSYECLKADVVITAGITKIPGSKDKWSRMDLLPVNIKIMREVGAIAKSY 121
Db 62 -GFSTSDSSNYKNMEGSDVIVVTAGMARKPG-----MSREDLFDKNVEIADVSKNIKY 115
QY 122 CPNAPVINITNPLDVMAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDVG 181

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Db 116 SPDSIIIVVSNPADIMAYALQKISGVDQPRIMGLGSLDSSRPTFLAKELDVSVEDVNA 175
Qy 182 MVIGVHGDMVPLSRYATVNGIPLSEFVKKGWIKOBEVDDIVOKTKVAGGEIVRLGQGS 241
Db 176 FVIGGHGDMVFPFIRYSSVAGIPIEKLLPK-----EKIDAIVKTRFGGGEIVNYLKAGS 230
Qy 242 AYYAPGASAIQMAESYLKDKRVMVSCYLOGQ-----YGVQNHVYLGVPVCVIGRGVEKII 297
Db 231 AYYAPGISITAMWESVINDKKRVIPCAAYITGKHAHYGINNKFIGVPIKIGERGVEEY 290
Qy 298 ELELTAQEROELOQSIDIV 316
Db 291 DIDFPEELELWKKSVASV 309

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Search completed: March 2, 2006, 19:45:39
Job time : 68 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 19:40:23 ; Search time 28 Seconds
(without alignments)
974.392 Million cell updates/sec

Title: US-09-390-846-2
Perfect score: 1688
Sequence: 1 MAVFEKTRPKIAVSGSMI.....GSIDVEMQKAIKALDASK 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 1688 | 100.0 | 330 | 2 | US-08-676-882-2 |
| 2 | 828 | 49.1 | 335 | 4 | PCT-US94-03796-2 |
| 3 | 706 | 41.8 | 329 | 1 | US-08-270-0138-2 |
| 4 | 706 | 41.8 | 329 | 1 | US-08-838-418-2 |
| 5 | 694 | 41.1 | 289 | 2 | US-09-902-540-13486 |
| 6 | 641 | 38.0 | 325 | 2 | US-09-134-001C-5533 |
| 7 | 464 | 27.5 | 324 | 2 | US-09-107-532A-6486 |
| 8 | 426 | 25.2 | 338 | 2 | US-09-134-000C-4417 |
| 9 | 412 | 24.4 | 317 | 1 | US-08-748-068-3 |
| 10 | 412 | 24.4 | 333 | 1 | US-08-748-068-1 |
| 11 | 406 | 24.1 | 354 | 2 | US-09-949-016-8002 |
| 12 | 405 | 24.0 | 351 | 2 | US-09-949-016-11252 |
| 13 | 405 | 24.0 | 351 | 2 | US-09-949-016-11253 |
| 14 | 401.5 | 23.8 | 322 | 2 | US-09-710-279-1412 |
| 15 | 401.5 | 23.8 | 322 | 2 | US-09-710-279-2384 |
| 16 | 401.5 | 23.8 | 330 | 2 | US-09-134-001C-4328 |
| 17 | 398 | 23.6 | 316 | 2 | US-09-830-230A-561 |
| 18 | 395.5 | 23.4 | 307 | 2 | US-09-107-532A-4274 |
| 19 | 391 | 23.2 | 333 | 1 | US-08-869-506-2 |
| 20 | 391 | 23.2 | 333 | 1 | US-09-128-967-2 |
| 21 | 390 | 23.1 | 333 | 1 | US-08-869-506-3 |
| 22 | 390 | 23.1 | 333 | 1 | US-09-128-967-3 |
| 23 | 389 | 23.0 | 331 | 2 | US-09-711-681-4 |
| 24 | 389 | 23.0 | 331 | 2 | US-10-274-266-4 |
| 25 | 388 | 23.0 | 331 | 2 | US-09-107-433-4752 |
| 26 | 388 | 23.0 | 332 | 2 | US-09-583-110-4591 |
| 27 | 377.5 | 22.4 | 327 | 1 | US-08-748-068-2 |

| | | | | | | |
|----|-------|------|-----|---|----------------------|-------------------|
| 28 | 371 | 22.0 | 295 | 2 | US-09-830-230A-562 | Sequence 562, App |
| 29 | 371 | 22.0 | 381 | 2 | US-09-711-681-2 | Sequence 2, Appli |
| 30 | 371 | 22.0 | 381 | 2 | US-10-274-266-2 | Sequence 2, Appli |
| 31 | 363 | 21.5 | 320 | 2 | US-09-535-381-2 | Sequence 2, Appli |
| 32 | 338 | 20.0 | 317 | 2 | US-09-489-039A-9794 | Sequence 9794, Ap |
| 33 | 285.5 | 16.9 | 205 | 2 | US-09-949-016-9136 | Sequence 9136, Ap |
| 34 | 277 | 16.4 | 339 | 2 | US-09-543-681A-5827 | Sequence 5827, Ap |
| 35 | 273.5 | 16.2 | 304 | 2 | US-09-634-238-238 | Sequence 238, App |
| 36 | 246.5 | 14.6 | 338 | 2 | US-08-922-957-3 | Sequence 3, Appli |
| 37 | 240 | 14.2 | 338 | 2 | US-08-922-957-1 | Sequence 1, Appli |
| 38 | 236.5 | 14.0 | 358 | 2 | US-09-248-796A-17253 | Sequence 17253, A |
| 39 | 231.5 | 13.7 | 298 | 2 | US-08-922-957-4 | Sequence 4, Appli |
| 40 | 225.5 | 13.4 | 262 | 2 | US-09-949-016-9135 | Sequence 9135, Ap |
| 41 | 225.5 | 13.4 | 262 | 2 | US-09-949-016-11622 | Sequence 11622, A |
| 42 | 224 | 13.3 | 333 | 2 | US-09-248-796A-17254 | Sequence 17254, A |
| 43 | 217 | 12.9 | 343 | 2 | US-09-248-796A-17252 | Sequence 17252, A |
| 44 | 212.5 | 12.6 | 322 | 2 | US-09-565-501A-112 | Sequence 112, App |
| 45 | 212.5 | 12.6 | 322 | 2 | US-09-639-206A-112 | Sequence 112, App |

ALIGNMENTS

RESULT 1
US-08-676-882-2
; Sequence 2, Application US/08676882
; Patent No. 6100241
; GENERAL INFORMATION:
; APPLICANT: Kok, Jacobus Johannes
; APPLICANT: van den Boogaart, Paul
; APPLICANT: Vermeulen, Arnoldus Nicolaas
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 6100241el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,882
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; TELEFAX: (301) 977-0847
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-676-882-2

| | | | | |
|-----------------------|-----------------|--|-----------|-------------|
| Query Match | 100.0% | Score 1688; | DB 2; | Length 330; |
| Best Local Similarity | 100.0% | Pred. No. 4e-177; | | |
| Matches 330; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | MAVFEKTRPKIAVSGSMIGGTMAFLCSIRLGLDVVLFDDVVPNMPMGKAMDISHNSVV | 60 | |
| DB | 1 | MAVFEKTRPKIAVSGSMIGGTMAFLCSIRLGLDVVLFDDVVPNMPMGKAMDISHNSVV | 60 | |
| QY | 61 | DTGITVYGSNVECLKGADVITAGITKIPGSKDEWSRMDLLPNVNIKIMREVGAIKS | 120 | |

Db 61 DTGITVGSNSYECLKGADVVIIITAGITKIPGSKDEKSRMDLLPVNIKIMREVGAAIKS 120
Qy 121 YCPNFAVINITNPLDVNVAALQESSGLPHHRIICGMAGMLDSSRRFRMIADKLEVSRRDVQ 180
Db 121 YCPNFAVINITNPLDVNVAALQESSGLPHHRIICGMAGMLDSSRRFRMIADKLEVSRRDVQ 180
Qy 181 GWIVGHGDMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLIGQG 240
Db 181 GWIVGHGDMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLIGQG 240
Qy 241 SAYYAPGASAIQMAESYLKDKRVMVCSYLOGQYGVQNHVYLGVPVCVIGRGVEKIEIE 300
Db 241 SAYYAPGASAIQMAESYLKDKRVMVCSYLOGQYGVQNHVYLGVPVCVIGRGVEKIEIE 300
Qy 301 LTAQEROELQGSIDEVKEMOKATAALDASK 330
Db 301 LTAQEROELQGSIDEVKEMOKATAALDASK 330
RESULT 2
PCT-US94-03796-2
; Sequence 2, Application PC/TUS9403796
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: GENE ENCODING THE LACTATE DEHYDROGENASE
; TITLE OF INVENTION: ENZYME OF PLASMODIUM FALCIPARUM
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03796
; FILING DATE: 06-APR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/046,160
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: DCI-066CPCC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-03796-2

Query Match 49.1%; Score 828; DB 4; Length 315;
Best Local Similarity 52.6%; Pred. No. 2.le-82;
Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSRLGDLVFLDVVPMMPMGKAMDISHNSSVDDTGTIVYG 68
Db 4 KAKIVLVGSGMIGVMTLIVQKNLGDVFLFDIVKMPHGKALDTSHTNVMAYSNCKVSG 63
Qy 69 SNSVECLKGADVVIIITAGITKIPGSKDEKSRMDLLPVNIKIMREVGAAIKSCPNAFVI 128
Db 64 SNTYDDLAGADVIVTAVGTAKPGSKDEKSRMDLLPVLNKIMETIGGHIKKNCNPAFII 123
Qy 129 NITNPLDVNVAALQESSGLPHHRIICGMAGMLDSSRRFRMIADKLEVSRRDVQGVGVHG 188
Db 124 VTNPDVDMVQLLHQHSGVPANKIIGLGGLDTSRLKYIISQKLVNCPVDVNAHIIVGAG 183
Qy 189 DHMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLIGQGSAYVAPGA 248
Db 184 NKWLLKRYITVGGIPLQEFINNNKLSDAELEAFDRTVNTALEIVNL--HASPYYVAPAA 241

Qy 249 SAIQMAESYLKDKRVMVCSYLOGQYGVQNHVYLGVPVCVIGRGVEKIEIELELTAEROE 308
Db 242 AIIEMAESYLKDKLVKVICSTLLEGQYHSDIFGGTPVVLGVANGVEQVIELQLNSEKAK 301
Qy 309 LOGSIDEVKEMQ 320
Db 302 FDEAIAETKRMK 313

RESULT 3
US-08-270-013B-2
; Sequence 2, Application US/08270013B
; Patent No. 5686294
; GENERAL INFORMATION:
; APPLICANT: Sogabe et al.
; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 61601-6780
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/270,013B
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 164701/1993
; FILING DATE: 02-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Robert F.
; REGISTRATION NUMBER: 27555
; REFERENCE/DOCKET NUMBER: 62321
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: (25)3533
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-270-013B-2

Query Match 41.8%; Score 706; DB 1; Length 329;
Best Local Similarity 45.3%; Pred. No. 6.2e-69;
Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;

Qy 9 RPKIAMVSGMIGTMAFLCSRLGDLVFLDVVPMMPMGKAMDISHNSSVDDTGTIV 66
Db 5 RKKISVIGAGTGAATTAFLAQKELGDVVLVDIPLQENPTKGKALDMLSEASPVLGPDANI 64
Qy 67 YGSNSVECLKGADVVIIITAGITKIPGSKDEKSRMDLLPVNIKIMREVGAAIKSCPNAF 126
Db 65 IGTSYDADTADSDIVVITAGIARKPG-----MSRDDLVTNNQKIMKQVTKVVVKYSPNCY 119
Qy 127 VTNITNPLDVNVAALQESSGLPHHRIICGMAGMLDSSRRFRMIADKLEVSRRDVQGVGV 186
Db 120 IIVLTPVDVMTYTVFKESGFPKRVIGSGVLDTRFTFVAEELNLSVKDVTGVVLGG 179
Qy 187 HGDHVMPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLIGQGSAYYAP 246
Db 180 HGDHVMPLVRYSVAGGIPLKLEIPK-----DRLDAIVERTRKGGGEIVNLLNGSAYYAP 234

Qy 247 GASAIQMAESYLKDRKRMVWSCVYQGYGVQNHVYLGVPVCVIGRGVKEKIELELTAQER 306
 Db 235 AASLVEMVEAILKQDRILPAIAYLEGEYGVGYLGVPTILGNGIEKIELELTAQER 294

RESULT 4

US-08-838-418-2
 ; Sequence 2, Application US/08838418
 ; Patent No. 574342
 ; GENERAL INFORMATION:
 ; APPLICANT: Sogabe et al.
 ; TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
 ; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
 ; STREET: Two Prudential Plaza, Suite 4900
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60601-6780.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,418
 ; FILING DATE: 17-MAR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 164701/1993
 ; FILING DATE: 02-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoover, Allen E.
 ; REGISTRATION NUMBER: 37354
 ; REFERENCE/DOCKET NUMBER: 78339
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 616-5600
 ; TELEFAX: (312) 616-5700
 ; TELEX: (25)3533
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 329 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-838-418-2

Query Match 41.8%; Score 706; DB 1; Length 329;
 Best Local Similarity 45.3%; Pred. No. 6.2e-69;
 Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;
 Qy 9 RPKIAMVSGMIGTMAFLCSLRELGDVVLFDV--VPNMPGKAMDISHNSVVDITGV 66
 Db 5 RKISVIGAGTGTATTAFLAQKELGDVVLVDIPQLENPTKGKALDLEASPVLGFDANI 64
 Qy 67 YGNSYSECLGADVVIITAGITKIPGSKDEKWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126
 Db 65 IGISDYADTADSDIVITAGIARKEPG-----MSRDDLVTNNQIMKQVTEVKVYSNCY 119
 Qy 127 VINITNPLDVMAALQESSGLPHHRICGMAGMLDSSFRFRMIADKLEVSPRDVGMYIGV 186
 Db 120 IIVLTNPVDAMTYTVFKESGFPKRVQSGVLDARFRTFAEELNISKVDVTGFLGG 179
 Qy 187 HGDHMYPLSYATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLIGOGSAYAP 246
 Db 180 HGDDMVPLVRSYAGGIPKLEIPK-----DRLDIAIVERTRKGGGEIVNLLGNSAYAP 234

Qy 247 GASAIQMAESYLKDRKRMVWSCVYQGYGVQNHVYLGVPVCVIGRGVKEKIELELTAQER 306
 Db 235 AASLVEMVEAILKQDRILPAIAYLEGEYGVGYLGVPTILGNGIEKIELELTAQER 294

RESULT 5

US-09-902-540-13486
 ; Sequence 13486, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 13486
 ; LENGTH: 289
 ; TYPE: PRT
 ; ORGANISM: Myxococcus xanthus
 ; US-09-902-540-13486

Query Match 41.1%; Score 694; DB 2; Length 289;
 Best Local Similarity 47.0%; Pred. No. 1.1e-67;
 Matches 140; Conservative 59; Mismatches 87; Indels 12; Gaps 3;
 Qy 6 KNTRPKIAMVSGMIGTMAFLCSLRELGDVVLFDV--VPNMPGKAMDISHNSVVDITG 63
 Db 2 QNGKKXIGLIGGGQIGGNLALLAVQSLGDVLYDIPAAEGLVKYKALDINQLAAVDGYD 61
 Qy 64 ITVGSNSYECLGADVVIITAGITKIPGSKDEKWSRMDLLPVNIKIMREVGAAIKSYCP 123
 Db 62 CRVKGTTDKVDAGSDVVIITAGMPPKPG-----MSREDLLEINLKIMTMDVAGNIKQHP 116
 Qy 124 NAFVINTNPLDVMAALQESSGLPHHRICGMAGMLDSSFRFRMIADKLEVSPRDVGOMV 183
 Db 117 NAFVINVAPLDANVFAHKKIAGLPKHMVAGMAGVLDTSRKFCEVAELGCSIRDVEALV 176
 Qy 184 IGVDHMYPLSYATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLIGOGSAY 243
 Db 177 LGGHGDDMVPLVRHRTVGGVPLTELAK-----DKLDAIIKRTREGGPELVGLYKTSAY 231
 Qy 244 YAPGASAIQMAESYLKDRKRMVWSCVYQGYGVQNHVYLGVPVCVIGRGVKEKIELEL 301
 Db 232 FGPAACAIAMAESFLQDRKRVLPAAALLEGQYINGYFVGVPVQIGAGGVKEKIHVEL 289

RESULT 6

US-09-134-001C-5533
 ; Sequence 5533, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 5533
 ; LENGTH: 325
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5533

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 38.0% | Score 641; | DB 2; | Length 325; |
| Best Local Similarity | 41.6%; | Pred. No. 8.8e-62; | | |
| Matches 132; | Conservative 71; | Mismatches 102; | Indels 12; | Gaps 4; |

| | | | |
|----|-----|--|-----|
| Qy | 9 | RPKIAMVSGMIGCTMAFLCSRLRELGDVLPFD--VVPNMPMGKAMDISHNSVVDTGITV | 66 |
| Db | 16 | RRKLSIIIGAGHTGTTAFILAQKELGDVILIERQQSGMAKGKALDILSGPIWGFTDSV | 75 |
| Qy | 67 | YGSNSYBCLKGADVVIITAGITTKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAF | 126 |
| Db | 76 | HGSVNIEDIKSDIVVMTAG--IPRKS--MTRIELVQTNQIEVRETALQIATYAPHSI | 130 |
| Qy | 127 | VINTNPLDVNVAALQSSGLPHRHICMAGMLDSSRPFRMIADKLEVPSPDVQGMVIGV | 186 |
| Db | 131 | IIVLTNPVDVMTYAFKASGPKPERRIIQSGILDAAARYRTFIAOELNVSVKDVNGFVLGG | 190 |
| Qy | 187 | HGDHWPVLSRVATVNGIPLSEFVKKGWIKQEEVDIIVQKTKVAGGEIVRLIGQSAYYAP | 246 |
| Db | 191 | HGDTMLPLINNTHTNGIPIV-----KHLISEBKIDOI VERTRKGAIEIALLIGQSAYYAP | 245 |
| Qy | 247 | GASAIQMAESYLKDRKRVWCVCSQLQOGYGVQNNHYLGPVCPVIGRGVKEIKIELELTQAQR | 306 |
| Db | 246 | ATAIYETIDAFNDRKLLPSIAYLEGEYGCSDICFGVPTIIGVQGIETKIEIVDMNDEY | 305 |
| Qy | 307 | QELQSGIDEVKEMQKAI | 323 |
| Db | 306 | QLOHSAQAVSEVKNSL | 322 |

RESULT 7

US-09-107-532A-6486
; Sequence 6486, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GPC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6486:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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, HYPOTHETICAL: YES
, ORIGINAL SOURCE:
, ORGANISM: Enterococcus faecium
, FEATURE:
, . NAME/KEY: misc feature
, LOCATION: (B) LOCATION 1...324
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US-09-107-532A-6486
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| Qy | 3 | VFEKTRPKIAMYGSMIGGTGMAFLCSRL | L-GDVVLFDVVVNNPMGKAMDISHNSSVD | 61 | | | |
| Db | 9 | LFMKTSRKVVIVGTGFVGTSTIAYMINQGISNELVLIDVNOEKAEGEALLDGMANGD | 68 | | | | |
| Qy | 62 | TGTVTVGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLFPVNIKIMREVGAAIKSY | 121 | | | | |
| Db | 69 | ENVAVW-SGGYBECKDADIVVITAGINQKPGQ---- | SRDLVKTNASIMRQIVKEIMGS | 122 | | | |
| Qy | 122 | CPNAFVINTNPLDVMAALQESSGELPHHRI | CGMAGMLDSRRFRMTADKLEVS | PRDVG | 181 | | |
| Db | 123 | GFGDIIIVASNPNVDIITYIAWNESSGLPTSRVIGTGTTLTTRPRKEIALKLKVDPRSVHG | 182 | | | | |
| Qy | 182 | MVLGVGHDMVPLSRVATYNGIPLSEFVKGW-I | KQEEVDIIVOKTKVAGGEIVRLLGQ | 240 | | | |
| Db | 183 | YIIGEHGDSVAWSHTTGVGKGVFEIVEKDHR | IAQDELVIDADKVRNAAYEIID-- | RKK | 240 | | |
| Qy | 241 | SAYYAPGASAIQMAEYSIKDKRKVMVCSY | CLQQGYGQNHYLGPVPCVIGRGVKEKIELE | 300 | | | |
| Db | 241 | ATYYGIGMSTARIVKAILNNEQAVLPVS | ALTYLTGEYDEKDIFTGVPISVDENGVR | EVVELS | 300 | | |
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RESULT 8

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US-09-134-000C-4417
; Sequence 4417, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynv Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134, 000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055, 778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4417
; LENGTH: 318
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US-09-134-000C-4417

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| Db | 2 | MKVFNK----KVAII GTGFVGTSIAY--SMINQIANELI | VDIDRAKSEGETDLDGV | 55 |
| Qy | 58 | SVYDTGITVGSNSYCLKGADVITAGTTKIPGSKDEWSRMDLLP | VNIKIMREVCAA | 117 |
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| Db | 56 | SWQGENVNWAGDYQNC-QNAVIVITAGANQPGQ---- | SRLDLVS INAEIMKTIVNN | 109 |
| Qy | 118 | IKSYCNPAFVINITNPDLVNMVAALQSSGLPHHRI CGMAGMLDSSRPRRMIA | KLEVS PR | 177 |
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| 110 | IMKSGFDGILVITASNPVDVLTVVAQASGLPVSTIIIGTGTTLDTTRPRKLSORLAIDPR | 169 |
| 178 | DVOQMVIYGHGDMHVPGLSRATVNGIPLSEFV-KKGMIKQBEVDVDIYQKTKVAGGIVRL | 236 |
| 170 | NVHGIIIGEHGDESEVAVWSHTMIGTKPILEIVDTTERLTSDDLLPIISDKVNTAYEIID- | 228 |
| 237 | LGGGSAYYAPGASATQMAESYLKDKRVMVCSYLGQYGVQNHVYLGVPVCGIGRGVEXI | 296 |
| 229 | -RKQATYYIGIMSTARIKVALINNEQAILPVSAVLDQYGGQDVFTGIPAVVQNGQVTDI | 287 |
| 297 | IELELTAQRERQELQGSIDEVEMQKAI | 323 |
| 288 | -IELNLAAEKELFOKSVTLQKQVMASL | 314 |

RESULT 9

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US-08-748-068-3
; Sequence 3, Application US/08748068
; Patent No. 5770410
; GENERAL INFORMATION:
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; APPLICANT:
;
; TITLE OF INVENTION: Chiral Synthesis
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; NUMBER OF SEQUENCES: 15
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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; APPLICATION NUMBER: US/08/748,068
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; FILING DATE: 12-NOV-1996
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; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/256,959
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; FILING DATE: 05-OCT-1994
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; APPLICATION NUMBER: GB 92 02033.8
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; FILING DATE: 30-JAN-1992
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; PRIOR APPLICATION DATA:
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; FILING DATE: 04-MAR-1992
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; APPLICATION NUMBER: GB 93/00204
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74 US-08-748-068-3

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| Qy | 5 | EKNTRPKIAMVGMGMIGTGAFLCSLRELGD-VVLFDPVPMMPGKAMDISHNSVVDTG | 63 | | |
| Db | 2 | KNNGGARVVVIGAGFVGASVVFALMNGQIADEIVLIDANESKAIGDAMDHNHGKVFAPKP | 61 | | |
| Qy | 64 | ITVYGSNSYELGADVVIITAGITKIPGSKDEWSBMDLLPVNIKIMREVGAIAKSYCP | 123 | | |
| Db | 62 | VDIWHGDDYDC-RDADLVITCAGANQKPGE-----TKLDLVDRKNIAFRSIVESVMAAGF | 115 | | |
| Qy | 124 | NAFVINITNPDLVWVAALOBSSGLPHHRI CGMAGMLDSSRRFMIADKLEVSPRDVGMV | 183 | | |

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Qy 184 IGWGDHVMPLSRVATVNGIPLSEFVK-KGWIQBEVDDIVQTKVAGGSEIVRLGGSSA 242
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Db 176 IGEHGDTELPVMSQAYIGVMPIRKLVBESKGEAQKOLERFVNVVDAAYQIIE--KKGAT 233
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Qy 243 YYAPGASAIQMAESYLKDRKVMVCSYLOGVQNHVYLGVPVIGGRCVEXKIELELT 302
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Db 234 YYGIAMGLARVTRAILHNEAILTVSAYLDGLYGERDVYIGVPAVINRNGIREVIEELN 293
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Qy 303 AQERQELQGSIDEVKEM 319
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Db 294 DDEKNRPHHSAATLKSV 310
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RESULT 10
US-08-748-068-1
; Sequence 1, Application US/08748068
; Patent No. 5770410
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Chiral Synthesis
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,068
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,959
; FILING DATE: 05-OCT-1994
; APPLICATION NUMBER: GB 92 02033.8
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 04702.6
; FILING DATE: 04-MAR-1992
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; INFORMATION FOR SEQ ID NO: 1:
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; Query Match 24.4%; Score 412; DB 1; Length 333;
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; Matches 101; Conservative 73; Mismatches 130; Indels 34; Gaps 10;
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; Qy 5 EKNTRP--KIAMVSGMIGGTMAFLCSLRELG-----DVVLFDVVVPMMPMGKAMDISHNS 57
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; Qy 58 SVVDTGITVYGSNVECLKGADWIIITAGITIKPGSKDEWSRMDLLPVNIKIMREVGA 117
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; Query Match 24.4%; Score 412; DB 1; Length 333;
; Best Local Similarity 29.9%; Pred. No. 1.6e-36;
; Matches 101; Conservative 73; Mismatches 130; Indels 34; Gaps 10;
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QY 178 DVQGMVIGVGHDMVPLSRVATVNGIPLSEF-----VKKGWIKOEVEDDIIQKTKVA 229
Db 184 SCHWILGERHGDSSVAVWGVNAGVSLQQLNPMGTNDSENW---KEVHKWVESAY- 239
QY 230 GGEIVRLGOGSAYYAPGASAIQMAESYLKDRKRVWVCSCYLOQYGVQNH-YLGVPCVI 288
Db 240 --EVKLU--KGYTNWAGLSVADLIESMLKSLRIHPVSTWVGMYGIENEVFLSLPCL 295
QY 289 GGRGVEKIELELTAQERQELQSGIDDEVKEMQKAIAL 326
Db 296 NARGLTSVINQKLDKDEVAQLKNSADTLWGIQDKLDL 333
RESULT 11
US-09-949-016-8002
; Sequence 8002, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8002
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8002
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Best Local Similarity 29.3%; Pred. No. 7.8e-36;
Matches 99; Conservative 75; Mismatches 130; Indels 34; Gaps 10;
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Db 35 EEAATVPNNKITVVGQGVG---MACAISILGKSLADELALVDVLDKLGEMMDLQHGS 90
QY 58 SVVDGTITVYGSNYECLKADVVITAGITKIPGSKDSESRMDLLPVNIKIMRVGAA 117
Db 91 LFLQTP--KIVADKDYSTANSKIIVVTVAGVQOEGE-----SRNLVQRNVNVFKFIPO 144
QY 118 IKSCYPNAPVINITNPLDVMVAALQESSGLPHRIGCMAGMLDSSRRFRMIADKLEVS 177
Db 145 IVKSPDCIIIVSNPVDILTIVTWKLSGLPKHRVIGSGCNDLSARFYLMAEKLGHPS 204
QY 178 DVQGMVIGVGHDMVPLSRVATVNGIPLSEF-----VKKGWIKOEVEDDIIQKTKVA 229
Db 205 SCHWILGERHGDSSVAVWGVNAGVSLQQLNPMGTNDSENW---KEVHKWVESAY- 260
QY 230 GGEIVRLGOGSAYYAPGASAIQMAESYLKDRKRVWVCSCYLOQYGVQNH-YLGVPCVI 288
Db 261 --EVKLU--KGYTNWAGLSVADLIESMLKSLRIHPVSTWVGMYGIENEVFLSLPCL 316
QY 289 GGRGVEKIELELTAQERQELQSGIDDEVKEMQKAIAL 326
Db 317 NARGLTSVINQKLDKDEVAQLKNSADTLWGIQDKLDL 354
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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Best Local Similarity 30.9%; Pred. No. 1e-35;
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QY 5 EKTRPKIAMVSGMIGTMAFLCSLRELCD--VVFVDPVPMMPKAMDISHNSVVDTG 63
Db 35 DENSQCKITIVGTGAVGMACAISILKDLADELALVDVLDKLGEMMDLQHGSFFSTS 94
QY 64 ITVYGSNYECLKADVVITAGITKIPGSKDSESRMDLLPVNIKIMRVGAAIKSYCP 123
Db 95 KITSGKD--YVSANSRIVIVTAGARQOEGE-----TLALVQRNVNVAIKSIIPAIVHYS 148
QY 124 NAFVINITNPLDVMVAALQESSGLPHRIGCMAGMLDSSRRFRMIADKLEVS 183
Db 149 DCKILVSNPVDILTIVTWKLSGLPKHRVIGSGCNDLSARFYLIGEBKLVHPTSCHGI 208
QY 184 IGVGHDMVPLSRVATVNGIPL-----SEFVKGWIKOEVEDDIIQKTKVAGGIVR 235
Db 209 IGEHGDSSVPLWSGVNVAGVALKTLDPKLTGSDSDEKHW-----KNHKQVIOSEYBIK 262
QY 236 LLQGSAYYAPGASAIQMAESYLKDRKRVWVCSCYLOQYGVQNH-YLGVPCVIGGRGVE 294
Db 263 LKGYTS--WAGLSVMDLVGSLKLRVRHPVSTWVGKLYGIBELFLSIPCLVGRNGVS 320
QY 295 KIIELELTAQERQELQSGIDDEVKEMQK 321
Db 321 DVVKINLSEEAALFKKSAETLWNIQK 347
RESULT 13
US-09-949-016-11253
; Sequence 11253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11253
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11253

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:38:02 ; Search time 109 Seconds
(without alignments)
2136.003 Million cell updates/sec

Title: US-09-390-846-2

Perfect score: 1688

Sequence: 1 MAVFEKTRPKIAVGSGL.....GSIDEVKEKQKAIALDASK 330

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|--------|---------------|--------|--------------|---------------------|
| 1 | 1688 | 100.0 | 330 | Q818U5_EIMAC | Q818U5 eimeria ace |
| 2 | 1398 | 82.8 | 330 | Q818U3_EIMMA | Q818U3 eimeria max |
| 3 | 1266 | 75.0 | 331 | Q818U4_EIMTE | Q818U4 eimeria ten |
| 4 | 1072 | 63.5 | 326 | LDH_TOXGO | Q27797 toxoplasma |
| 5 | 1041.5 | 61.7 | 329 | P90613_TOXGO | P90613 toxoplasma |
| 6 | 905.5 | 53.6 | 316 | Q6DQ12_TOXGO | Q6DQ12 toxoplasma |
| 7 | 889 | 52.7 | 330 | Q720X7_BABBO | Q720X7 babesia bov |
| 8 | 886.5 | 52.5 | 320 | MDH_RHLV | O33525 rhizobium l |
| 9 | 881 | 52.2 | 316 | Q4PRK9_PLAVI | O4PRK9 plasmodium |
| 10 | 877.5 | 52.0 | 320 | MDH_BRHE | O591m0 bartonella |
| 11 | 876.5 | 51.9 | 320 | MDH_BRUME | O8y7e7 brucella me |
| 12 | 873.5 | 51.7 | 320 | MDH_AGR75 | Q7cwk7 egrobacteri |
| 13 | 873.5 | 51.7 | 320 | MDH_RHIME | Q9ey76 rhizobium m |
| 14 | 870.5 | 51.6 | 320 | MDH_BARQU | Q6fyd0 bartonella |
| 15 | 868.5 | 51.5 | 320 | MDH_BRUAJ | O57ax1 brucella ab |
| 16 | 868 | 51.4 | 322 | MDH_BRUAJ | O89x59 bradyrhizob |
| 17 | 863.5 | 51.2 | 320 | MDH_BRUSU | Q8fyf4 brucella su |
| 18 | 862.5 | 51.1 | 322 | MDH_RHOFA | P80458 rhodospseudo |
| 19 | 862.5 | 51.1 | 324 | Q4TP00_9SPHN | Q4TP00 erythroba |
| 20 | 862 | 51.1 | 322 | MDH_RHIL0 | Q98ec4 rhizobium l |
| 21 | 851.5 | 50.4 | 320 | MDH_METEX | Q84f58 methylobact |
| 22 | 851.5 | 50.4 | 320 | MDH_SILPO | O51xel silicibacte |
| 23 | 850.5 | 50.4 | 320 | MDH_CAUCR | Q3a2b1 caulobacter |
| 24 | 847 | 50.2 | 299 | Q6JH30_PLAVI | Q6JH30 plasmodium |
| 25 | 846.5 | 50.1 | 314 | MDH_RICCN | Q7pbn3 rickettsia |
| 26 | 837.5 | 49.6 | 314 | MDH_RICCN | Q92ia0 rickettsia |
| 27 | 836 | 49.5 | 316 | Q7RHU8_PLAYO | Q7RHU8 plasmodium |
| 28 | 835 | 49.5 | 299 | Q6JH31_PLAMA | O6ih31 plasmodium |
| 29 | 833 | 49.3 | 316 | Q4Z783_PLABE | Q4Z783 plasmodium |
| 30 | 833 | 49.3 | 322 | Q7S197_PLABE | Q7S197 plasmodium |
| 31 | 831.5 | 49.3 | 316 | LDH1_PLAPD | Q27743 plasmodium |

| | | | | | | |
|----|-------|------|-----|---|--------------|--------------------|
| 32 | 831.5 | 49.3 | 316 | 2 | Q5R2J8_PLARE | Q5R2J8 plasmodium |
| 33 | 831.5 | 49.3 | 316 | 2 | Q76NM3_PLAF7 | Q76NM3 plasmodium |
| 34 | 831.5 | 49.3 | 316 | 2 | Q71T02_PLAFA | Q71T02 plasmodium |
| 35 | 826.5 | 49.0 | 314 | 1 | MDH_RICPR | Q9zdf3 rickettsia |
| 36 | 826.5 | 49.0 | 314 | 1 | MDH_RICTY | O68wz8 rickettsia |
| 37 | 824 | 48.8 | 316 | 2 | O4XTG3_PLACH | O4xtg3 plasmodium |
| 38 | 822.5 | 48.7 | 314 | 1 | MDH_RICPE | Q4uly2 rickettsia |
| 39 | 810.5 | 48.0 | 316 | 1 | MDH_WOLPM | Q73944 wolbachia p |
| 40 | 808.5 | 47.9 | 316 | 1 | LDH_BOTBR | P93052 botryococcu |
| 41 | 808.5 | 47.9 | 316 | 1 | MDH_WOLTR | O5gt41 wolbachia s |
| 42 | 807.5 | 47.8 | 316 | 2 | O9BM13_PLAFA | O9bm13 plasmodium |
| 43 | 807 | 47.8 | 299 | 2 | O6JH32_9APIC | O6jh32 plasmodium |
| 44 | 806.5 | 47.8 | 317 | 1 | MDH_GEOSL | Q74d53 geobacter s |
| 45 | 805 | 47.7 | 321 | 2 | Q4N618_THEPA | Q4n618 theileria p |

ALIGNMENTS

RESULT 1

Q818U5_EIMAC
ID Q818U5_EIMAC PRELIMINARY; PRT; 330 AA.
AC Q818U5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lactate dehydrogenase.
GN Name=LDH;
OS Eimeria acervulina.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
OC Eimeria.
OX NCBI_TaxID=5801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schaap D.C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kok H.J., van den Boogaart P., Vermeulen A.N., Schaap D.C.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY143388; AAN38975.1; -; mRNA.
DR HSP; Q27743; ICET.
DR GO; GO:0004553; F:Hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
DR GO; GO:0004459; F:L-lactate dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR GO; GO:0006100; P:tricarboxylic acid cycle intermediate metab. . . ; IEA.
DR InterPro; IPR001089; Glyco_hydro_4.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR001557; L_LDH_MDH.
DR Pfam; PF02866; Ldh_1_C_1.
DR Pfam; PF00056; Ldh_1_N_1.
DR PIRSF; PIRSF000102; Lac_dehydrog; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR PRODOM; PD006892; Glyco_hydro_4; 1.
KW Oxidoreductase.
SQ SEQUENCE 330 AA; 35857 MW; 79500C3360E3A84C CRC64;

Query Match 100.0%; Score 1688; DB 2; Length 330;

Best Local Similarity 100.0%; Pred. No. 8.7e-120;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MAVFEKTRPKIAVGSGLGGTMAFLCSLRELGDVVLFDDVNNPMGKAMDISHNSVV | 60 |
| Db | 1 | MAVFEKTRPKIAVGSGLGGTMAFLCSLRELGDVVLFDDVNNPMGKAMDISHNSVV | 60 |
| Qy | 61 | DTGITVYGSNSYECLGADVVITAGITKIPGSKDKEWSEMDLLPVNIKIMREVGAIAKS | 120 |
| Db | 61 | DTGITVYGSNSYECLGADVVITAGITKIPGSKDKEWSEMDLLPVNIKIMREVGAIAKS | 120 |
| Qy | 121 | YCNAFVNITNPLDVNVAALQESSGLPHHRICMGAGMLDSSRFRRIADKLEVPDQV | 180 |
| Db | 121 | YCNAFVNITNPLDVNVAALQESSGLPHHRICMGAGMLDSSRFRRIADKLEVPDQV | 180 |

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Db      121 YCPNFAVINITNPLDVMVAALQESSGLPHHRIICGMAGMLDSSRRPRMIADKLEVSPRDVQ 180
Qy      181 GMVIGVGHDMVPLSRVATVNGIPLSEFVKKGWIKQBEVDDIVQKTKVAGGEIVRLLGQ 240
Db      181 GMVIGVGHDMVPLSRVATVNGIPLSEFVKKGWIKQBEVDDIVQKTKVAGGEIVRLLGQ 240
Qy      241 SAYYAPGASAIQMAESYLKDKRKVMVCSYLOGQYGVQNHVYLGVPVCGVIGRGVEKIELE 300
Db      241 SAYYAPGASAIQMAESYLKDKRKVMVCSYLOGQYGVQNHVYLGVPVCGVIGRGVEKIELE 300
Qy      301 LTAQERQELQGSIDEVKEMQKAIALDASK 330
Db      301 LTAQERQELQGSIDEVKEMQKAIALDASK 330

RESULT 2
Q818U3_EIMMA
ID      Q818U3_EIMMA PRELIMINARY; PRT; 330 AA.
AC      Q818U3;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Lactate dehydrogenase.
GN      Name=Ldh;
OS      Eimeria maxima.
OC      Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
OC      Eimeria.
OX      NCBI_TaxID=5804;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Schaap D.C.;
RL      Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      Nielsen R., Schaap D.C.;
RL      Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY143390; AAN38977.1; -, mRNA.
DR      HSSP; Q27743; 1CET.
DR      GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.
DR      GO; GO:0004459; F:L-lactate dehydrogenase activity; IEA.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      GO; GO:0006096; P:glycolysis; IEA.
DR      GO; GO:0006100; P:tricarboxylic acid cycle intermediate metab. . . ; IEA.
DR      InterPro; IPR001086; Glyco_hydro_4.
DR      InterPro; IPR001236; ldh.
DR      InterPro; IPR001557; L_LDH_MDH.
DR      Pfam; PF02866; Ldh_1_C; 1.
DR      Pfam; PF00056; Ldh_1_N; 1.
DR      PIRSF; PIRSF00102; Lac dehydrog; 1.
DR      PRINTS; PR00086; LDHDRGNASE.
DR      ProDom; PD006892; Glyco_hydro_4; 1.
KW      Oxidoreductase.
SQ      SEQUENCE 330 AA; 35951 MW; 380CB5B7151B59E8 CRC64;

Query Match 82.8%; Score 1398; DB 2; Length 330;
Best Local Similarity 80.6%; Pred. No. 9e-98;
Matches 266; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

Qy      1 MAVFEKNTRPKIAMVSGMIGTMAFLCSLRELGDVVLFDVVPNMPGKAMDISHNSVV 60
Db      1 MAVFEQNKRPKIALVSGMIGTMAFLCSLRELGDVVLFDVVPNMPGKAMDLCNNSVV 60

Qy      61 DTGITVYGSNSYECLGADVVIIITAGITKIPGSKDEWSRMDLLPVNIKIMREVGAAIKS 120
Db      61 DNGITVYGSNSYECLTNADVVIIITAGITKIPGSKDEWSRMDLLPVNIKIMREVGGAIKK 120

Qy      121 YCPNFAVINITNPLDVMVAALQESSGLPHHRIICGMAGMLDSSRRPRMIADKLEVSPRDVQ 180
Db      121 YCPNFAVINITNPLDVMVAALQESSGLPHHRIICGMAGMLDSSRLRMIADCLHVSHPDVQ 180

Qy      181 GMVIGVGHDMVPLSRVATVNGIPLSEFVKKGWIKQBEVDDIVQKTKVAGGEIVRLLGQ 240
Db      181 GMVIGVGHDMVPLSRVATVNGIPLSEFVKKGWIKQBEVDDIVQKTKVAGGEIVRLLGQ 240

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Db      181 GMVIGVGHDMVPLSRVATVNGIPIQEFINKGLINKKEINNIYNKTKQAGGDIVRLLGQ 240
Qy      241 SAYYAPGASAIQMAESYLKDKRKVMVCSYLOGQYGVQNHVYLGVPVCGVIGRGVEKIELE 300
Db      241 SAYYAPGTSAILMAESYLKDKRFLFVSSCYNGQYNNVNNHYLGVPCLIGGKGIEFIELD 300
Qy      301 LTAQERQELQGSIDEVKEMQKAIALDASK 330
Db      301 LNOEEKLLQGSIDEVLEMQKAIALDAGK 330

RESULT 3
Q818U4_EIMTE
ID      Q818U4_EIMTE PRELIMINARY; PRT; 331 AA.
AC      Q818U4;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Lactate dehydrogenase.
GN      Name=Ldh;
OS      Eimeria tenella.
OC      Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
OC      Eimeria.
OX      NCBI_TaxID=5802;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Schaap D.C.;
RL      Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      Arts G., Kroezen H., Schaap D.C.;
RL      Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: Belongs to the LDH/MDH superfamily. LDH family.
DR      EMBL; AY143389; AAN38976.1; -, mRNA.
DR      HSSP; Q27743; 1CET.
DR      GO; GO:0004459; F:L-lactate dehydrogenase activity; IEA.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      GO; GO:0006096; P:glycolysis; IEA.
DR      GO; GO:0006100; P:tricarboxylic acid cycle intermediate metab. . . ; IEA.
DR      InterPro; IPR001236; ldh.
DR      InterPro; IPR001557; L_LDH_MDH.
DR      Pfam; PF02866; Ldh_1_C; 1.
DR      Pfam; PF00056; Ldh_1_N; 1.
DR      PIRSF; PIRSF000102; Lac dehydrog; 1.
DR      PRINTS; PR00086; LDHDRGNASE.
KW      Oxidoreductase.
SQ      SEQUENCE 331 AA; 34965 MW; BEF87B9F837AE469 CRC64;

Query Match 75.0%; Score 1266; DB 2; Length 331;
Best Local Similarity 71.4%; Pred. No. 9.4e-88;
Matches 235; Conservative 51; Mismatches 43; Indels 0; Gaps 0;

Qy      1 MAVFEKNTRPKIAMVSGMIGTMAFLCSLRELGDVVLFDVVPNMPGKAMDISHNSVV 60
Db      1 MAVFEKVRPKIALVSGMIGTMAFLCSLRELGDVVLFDVVPNMPAGKALDLCHTAAVA 60

Qy      61 DTGITVYGSNSYECLGADVVIIITAGITKIPGSKDEWSRMDLLPVNIKIMREVGAAIKS 120
Db      61 DNGVRVQGANSYASLEGGADVIIITAGITKAAAGSKDQESRSKDLLPVNVTILREVGAIKQ 120

Qy      121 YCPNFAVINITNPLDVMVAALQESSGLPHHRIICGMAGMLDSSRRPRMIADKLEVSPRDVQ 180
Db      121 FCPHAFVINITNPLDVMVAALREAGLPAARVCGMAGVLDLSAFLRLLADRLGVSPRDVQ 180

Qy      181 GMVIGVGHDMVPLSRVATVNGIPLSEFVKKGWIKQBEVDDIVQKTKVAGGEIVRLLGQ 240
Db      181 AMVLGVGHDMVPLSRFATVNGVPLGELARQGWISEAETREVERQTRAGGDIVRLLGQ 240

Qy      241 SAYYAPGASAIQMAESYLKDKRKVMVCSYLOGQYGVQNHVYLGVPVCGVIGRGVEKIELE 300
Db      241 SAYFAFGAAVAAAEAYLLDKQKRVFVCSYLEGFYGVGRHCLGVPCVVGAGGVERVIELP 300

Qy      301 LTAQERQELQGSIDEVKEMQKAIALDAS 329

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Db 301 LDAREAQLOASIDEVREHMQLAADAA 329

RESULT 4

LDH_TOXGO

ID LDH_TOXGO STANDARD; PRT; 326 AA.

AC Q27797;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH).

OS Toxoplasma gondii.

OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;

OC Toxoplasma.

OX NCBI_TaxID=5811;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ME49;

RX MEDLINE=96123406; PubMed=8577343; DOI=10.1016/0166-6851(95)00069-D;

RA Yang S., Parmley S.F.;

RT "A bradyzoite stage-specifically expressed gene of Toxoplasma gondii encodes a polypeptide homologous to lactate dehydrogenase.";

RL Mol. Biochem. Parasitol. 73:291-294 (1995).

CC -|- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.

CC -|- PATHWAY: Anaerobic glycolysis; final step.

CC -|- SUBUNIT: Homotetramer (By similarity).

CC -|- SIMILARITY: Belongs to the LDH/MDH superfamily. LDH family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

DR EMBL; U23207; AAC4683.1; -; mRNA.

DR FDB; ISOV; X-ray; A/B=1-326.

DR PDB; ISOM; X-ray; A/B=1-326.

DR SMR; Q27797; 3-325.

DR InterPro; IPR011304; L-LDH-NAD.

DR InterPro; IPR001557; L-LDH_MDH.

DR InterPro; IPR001236; Ldh.

DR PANTHER; PTHR11540; Ldh; 1.

DR Pfam; PF02866; Ldh_1_C; 1.

DR Pfam; PF00056; Ldh_1_N; 1.

DR PIRSF; PIRSF000102; Lac_mal DH; 1.

DR PRINTS; PR00086; LLDHGRNASE.

DR PROSITE; PS00064; L_LDH; FALSE_NEG.

KW 3D-structure; Glycolysis; NAD; Oxidoreductase.

FT NP_BIND 39 60 NAD (By similarity).

FT ACT_SITE 186 186 Proton acceptor (By similarity).

FT BINDING 99 99 Substrate (By similarity).

FT BINDING 131 131 NAD or substrate (By similarity).

FT BINDING 162 162 Substrate (By similarity).

FT SEQUENCE 326 AA; 35307 MW; E692C95A81FC031E CRC64;

Query Match 63.5%; Score 1072; DB 1; Length 326;

Best Local Similarity 62.6%; Pred.No. 4.9e-73;

Matches 199; Conservative 56; Mismatches 63; Indels 0; Gaps 0;

QY 9 RPKIAMVSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDGTGITYG 68

DB 8 RKKIAMVSGMIGGTMAFLCSLRELGDVVLFDVVTGMPEGKALDSDQATSIADTVSVTS 67

QY 69 SNSYECLKAGADVVIITAGITKI PKGSKDEWSRMDLLPVNPKIMREVGAAIKSYCPNAFVI 128

DB 68 ANQYEKIAGSDVVIITAGITKVPKSGDEWSRMDLLPVNNAKIIRIEVAGGVKKYCPYAFVI 127

QY 129 NITNPLDVMVAALQSSGLPHHRI CGMAGMLDSSRFRMIAADKLEVS PRDVQGVVGHG 188

DB 128 VVTNPLDCMVKCFEASGLPKMVMCMANVLDSARFRFIADQLQLEISPRDIQATVITGH 187

QY 189 DHMVPLSRYATVNGIPLSEFVKKGWIKOEBEVDVDTQKTKVAGGIVRLLLGQGSAYYAPGA 248

Db 301 LDAREAQLOASIDEVREHMQLAADAA 329

RESULT 5

P90613_TOXGO

ID P90613_TOXGO PRELIMINARY; PRT; 329 AA.

AC P90613;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Lactate dehydrogenase (EC 1.1.1.27).

OS Toxoplasma gondii.

OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;

OC Toxoplasma.

OX NCBI_TaxID=5811;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ME49;

RX MEDLINE=97169139; PubMed=9016946; DOI=10.1016/S0378-1119(96)00566-5;

RA Yang S., Parmley S.F.;

RT "Toxoplasma gondii expresses two distinct lactate dehydrogenase homologous genes during its life cycle in intermediate hosts.";

RL Gene 184:1-12(1997).

CC -|- SIMILARITY: Belongs to the LDH/MDH superfamily. LDH family.

DR EMBL; U35118; AAC47443.1; -; mRNA.

DR PDB; 1PZE; X-ray; A=1-329.

DR PDB; 1PZF; X-ray; A/B/C/D=1-329.

DR PDB; 1PZG; X-ray; A/B/C/D=1-329.

DR PDB; 1PZH; X-ray; A/B/C/D=1-329.

DR GO; GO:0004459; F-L-lactate dehydrogenase activity; IEA.

DR GO; GO:0016491; F-oxalate dehydrogenase activity; IEA.

DR GO; GO:0006096; P-glycolysis; IEA.

DR GO; GO:0006100; P-tricarboxylic acid cycle intermediate metab. .; IEA.

DR InterPro; IPR001236; Ldh.

DR InterPro; IPR001557; L-LDH_MDH.

DR Pfam; PF02866; Ldh_1_C; 1.

DR Pfam; PF00056; Ldh_1_N; 1.

DR PIRSF; PIRSF000102; Lac dehydrog; 1.

DR PRINTS; PR00086; LLDHGRNASE.

KW Oxidoreductase.

SQ SEQUENCE 329 AA; 35548 MW; F06387B5AC0E6BBB CRC64;

Query Match 61.7%; Score 1041.5; DB 2; Length 329;

Best Local Similarity 60.4%; Pred.No. 1e-70; 71; Indels 1; Gaps 1;

Matches 194; Conservative 55; Mismatches 71; Indels 1; Gaps 1;

QY 9 RPKIAMVSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSSVVDGTGITYG 68

DB 9 RKKIAMVSGMIGGTMAFLCSLRELGDVVLFDVVTGMPEGKALDSDQATSIADTVSVTS 67

QY 69 SNSYECLKAGADVVIITAGITKI PKGSKDEWSRMDLLPVNPKIMREVGAAIKSYCPNAFVI 127

DB 68 ANQYEKIAGSDVVIITAGITKVPKSGDEWSRMDLLPVNNAKIIRIEVAGGVKKYCPYAFVI 127

QY 129 NITNPLDVMVAALQSSGLPHHRI CGMAGMLDSSRFRMIAADKLEVS PRDVQGVVGHG 188

DB 128 VVTNPLDCMVKCFEASGLPKMVMCMANVLDSARFRFIADQLQLEISPRDIQATVITGH 187

QY 189 DHMVPLSRYATVNGIPLSEFVKKGWIKOEBEVDVDTQKTKVAGGIVRLLLGQGSAYYAPGA 248

Db 301 LDAREAQLOASIDEVREHMQLAADAA 329

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Db      249 ASAVAMATSFNLDKRVPCSVYCNGBVGLKDMFGLPAVIGGAGIERVIELELNEBEKK 308
Qy      308 ELQGSIDEVEMQKAIALDA 328
Db      309 QFQKSVDDVNALNKAVAAQA 329

RESULT 6
Q6DQL2_TOXGO
ID      Q6DQL2_TOXGO PRELIMINARY; PRT; 316 AA.
AC      Q6DQL2;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE      Malate dehydrogenase.
OS      Toxoplasma gondii.
OC      Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC      Toxoplasma.
OX      NCBI_TaxID=5811;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=RH;
RC      Shen C., Zhan X., He A., Li Z.;
RA      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
[2]
RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=RH;
RC      PubMed=14598170; DOI=10.1007/s00436-003-0996-1;
RX      Chan M., Sim T.S.;
RA      "Functional characterization of an alternative (lactate dehydrogenase-
RT      like) malate dehydrogenase in Plasmodium falciparum.";
RL      Parasitol. Res. 92:43-47(2004).
[3]
RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=RH;
RC      Shen C., Zhan X., Zheng X., Zheng B., He A., Li Z., Zheng H.;
RT      "Cloning and characterization of the malate dehydrogenase gene from
RT      Toxoplasma gondii.";
RL      Zhongguo Ren Shou Gong Huan Bing Za Zhi 21:0-0(2005).
DR      EMBL; AY650028; AAT67462.1; -; mRNA.
DR      EMBL; AY972525; AAX83280.1; -; Genomic DNA.
DR      GO; GO:0004459; F:l-lactate dehydrogenase activity; IEA.
DR      GO; GO:0030060; F:l-malate dehydrogenase activity; IEA.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      GO; GO:0006096; P:glycolysis; IEA.
DR      GO; GO:0006108; P:malate metabolism; IEA.
DR      InterPro; IPR001236; ldh.
DR      InterPro; IPR001557; L_LDH_MDH.
DR      InterPro; IPR011275; MalateDH_bact.
DR      Pfam; PF02866; Ldh_1_C; 1.
DR      Pfam; PF00056; Ldh_1_N; 1.
DR      PIRSF; PIRSF00102; Lac dehydrog; 1.
DR      PRINTS; PRO0086; LLDHDRGNASE.
DR      TIGRfams; TIGR01763; MalateDH_bact; 1.
SQ      SEQUENCE 316 AA; 33777 MW; 10361A049B71D559 CRC64;

Query Match 53.6%; Score 905.5; DB 2; Length 316;
Best Local Similarity 54.9%; Pred. No. 2.1e-60;
Matches 173; Conservative 57; Mismatches 80; Indels 5; Gaps 1;

Qy      8 TRPKIAMVSGMTGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSVVDGTGITY 67
Db      2 SRRKIGLIGNICATLALLSAVKELGDVNVFVVDLPQKCLDLVLTPIGSDVRF 61
Qy      68 GSNSEYCLKGADVVIITAGITKIPGSKDKEWSRMDLLPVNVIKIMREYGAIAKSCYCPN 127
Db      62 GSNDSYVLKQADVLIITAGVPRKEG-----MSRDDLLAIINAKINGQVGEAIKQYCPN 116
Qy      128 INTNPLDVMVAALQESSGLPHHRIICMAGMLDSSRRFRMIADKLEVPDRDQGMVIGVH 187
Db      117 ICITNPLDVMVYILREKCGLPHPKVCVMAGVLD SARLRTFLSERLNVSVDDIHALVMG 176
Qy      188 GDHMPVLSRYATVNGIPLSEFVKGWIKQBEVDVIVQTKVAGGEIVRLIGQGSAYYAPG 247

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Db      177 GDTWVPLPRTTIVGGIPLPELVKGMISQEVDDIVQTRNGGGEIVSLKTKGSAFFAPA 236
Qy      248 ASAIQMAESYLDKDRKRMVSCYLCQYGVQNHLYGVPCVIGGRGVKEKIELELTAQERQ 307
Db      237 AAGVMAEAYLKDREKVLPCAAYLNGEYGVKQMYGVGVCVIGAGGVKEKIVELDLTPEEK 296
Qy      308 ELQGSIDEVEMQKA 322
Db      297 MPERSVESVKTLIAA 311

RESULT 7
Q7ZOX7_BABBO
ID      Q7ZOX7_BABBO PRELIMINARY; PRT; 330 AA.
AC      Q7ZOX7;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      L-lactate dehydrogenase.
GN      Names=BLDH;
OS      Babesia bovis.
OC      Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX      NCBI_TaxID=5865;
[1]
RN      NUCLEOTIDE SEQUENCE.
RP      Bork S., Okamura M., Boonchit S., Hirata H., Yokoyama N., Igarashi I.;
RT      "Identification of Babesia bovis L-lactate dehydrogenase as a
RT      potential chemotherapeutic target against bovine babesiosis.";
Mol. Biochem. Parasitol. 136:165-172(2004).
CC      -l- SIMILARITY: Belongs to the LDH/MDH superfamily. LDH family.
DR      EMBL; AB112429; BAC77691.1; -; mRNA.
DR      HSSP; Q27743; ICET.
DR      GO; GO:0004459; F:l-lactate dehydrogenase activity; IEA.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      GO; GO:0006096; P:glycolysis; IEA.
DR      GO; GO:0006100; P:tricarboxylic acid cycle intermediate metab. .; IEA.
DR      InterPro; IPR001236; ldh.
DR      InterPro; IPR001557; L_LDH_MDH.
DR      Pfam; PF02866; Ldh_1_C; 1.
DR      Pfam; PF00056; Ldh_1_N; 1.
DR      PIRSF; PIRSF00102; Lac dehydrog; 1.
DR      PRINTS; PRO0086; LLDHDRGNASE.
DR      OXidoreductase.
KW      SEQUENCE 330 AA; 35544 MW; 3004F52502B739EC CRC64;

Query Match 52.7%; Score 889; DB 2; Length 330;
Best Local Similarity 52.7%; Pred. No. 3.9e-59;
Matches 166; Conservative 62; Mismatches 87; Indels 0; Gaps 0;

Qy      9 RPKIAMVSGMTGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSVVDGTGITYG 68
Db      15 RNKISLIGSGNIGGVNAYLAQLKELGDVVLFDIAPKLGAAKALDIHANAITYDTSQNVIG 74
Qy      69 SNSYECLKGADVVIITAGITKIPGSKDKEWSRMDLLPVNVIKIMREYGAIAKSCYCPN 128
Db      75 TTSYEDIAGSDVCIITAGLAKUPNKSDDSDSDLDLVPAPNSKINFTIGENIKKYAPN 134
Qy      129 NITNPLDVMVAALQESSGLPHHRIICMAGMLDSSRRFRMIADKLEVPDRDQGMVIGVH 188
Db      135 CITNPLDVMVLMKLTGTGPKNVVGMGGLDSSRMCHYIADKLRVNPVYVHSGCIGHG 194
Qy      189 DHMPVLSRYATVNGIPLSEFVKGWIKQBEVDVIVQTKVAGGEIVRLIGQGSAYYAPGA 248
Db      195 DSMIPLTNHTVNGIPIQRIEFGITQAEIDKRIABERTIGSGMELVQLYNGSAFFAPAT 254
Qy      249 SAIQMAESYLDKDRKRMVSCYLCQYGVQNHLYGVPCVIGGRGVKEKIELELTAQERQ 308
Db      255 AAIEMASAYLSDKRSVIVCSYLEGEGYHNDVLTGTPAIIANGIEKIIITKLUSAEQAK 314
Qy      309 LOGSIDEVEMQKAI 323
Db      315 LDASVKEIRLEALV 329

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[illegible]

```
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37).
GN Name=mdh; OrderedLocusNames=BHI6570;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=39323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alamar U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvt M.,
RA La Scoia B., Holmberg M., Anderson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
CC -1- FUNCTION: Catalyzes the reversible oxidation of malate to
CC oxaloacetate (By similarity).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -1- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ENBL; BX997699; CAP28418.1; -; Genomic_DNA.
DR HAMAP; MF 00487; -; 1.
DR InterPro; IPR001557; 1. LDH_MDH.
DR InterPro; IPR001236; 1dh.
DR InterPro; IPR011275; MalatedH_bact.
DR PANTHER; PTHR11540; 1dh; 1.
DR Pfam; PF02866; Ldh_1_C; 1.
DR Pfam; PF00056; Ldh_1_N; 1.
DR PIRSF; PIRSF000102; Ldh_mal_DH; 1.
DR PRINTS; PR00086; LLDHDSGNASE.
DR TIGRFAMs; TIGR01763; MalatedH_bact; 1.
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.
FT ACT_SITE 149 149 Proton relay (By similarity).
FT ACT_SITE 176 176 Proton relay (By similarity).
FT BINDING 83 83 Substrate carboxyl (By similarity).
FT BINDING 89 89 Substrate carboxyl (By similarity).
FT BINDING 152 152 Substrate carboxyl (By similarity).
SQ SEQUENCE 320 AA; 33664 MW; 24C2AF4A2A2C720 CRC64;

Query Match 52.0%; Score 877.5; DB 1; Length 320;
Best Local Similarity 52.8%; Pred. No. 2.8e-58;
Matches 168; Conservative 66; Mismatches 79; Indels 5; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSRLGDLVFLFDVVPNPMGMKAMDISHNSVVDGTITVG 68
DB 3 RKKIALGSGMIGTMAFLCSRLGDLVFLFDVVPNPMGMKAMDISHNSVVDGTITVG 62
QY 69 SNSYECLKADVVIITAGITKIPGSKDKEWSRMDLLFPVNIKIMREYGAAIKSYCPNAFVI 128
DB 63 ANSYDVIEGADVVIITAGVARKPG-----NSRDLLGLNLKWMQVQAGIKKYASSAFVI 117
QY 129 NITNPLDVMVAALQESSGLPHRRCGMAGMLDSSRFRMTADKLEVSFRDQGVVIGVHG 188
DB 118 CITNPLDAMVWALQKFSGLPTQKVVGMAGILDSARFHFLEEFKISVKDVTAPVLGGHG 177
QY 189 DHMPLSRYATVNGIPLSFSEVKKWKIQQEVEDDITVQTKVAGGIVLRLGGSGAYYAPGA 248
DB 178 DSMVPLVRYSTVGISLPDLVGMGWTTOEKIDQIIQTRDGGABIVSLKTSYAFYAPAA 237
QY 249 SAIQMAESYLKDRKRVVMVCSYQGGYGVQVNHLYGVPCVIGGRGVEKIIIELETAQRQE 308
DB 238 SAVSMAEAYLKDRKRVVVAAYLSSQYGVKDYTVGVVPVWIGAGGVERVIBIDLKBEKAA 297
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QY 309 LOGSIDVEKEMOKATAAL 326
DB 298 FEKSVSQVQLCEACIAV 315

RESULT 11
MDH_BRUME STANDARD; PRT; 320 AA.
AC Q8YJ57;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37).
GN Name=mdh; OrderedLocusNames=BMEI0137;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756888; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapratil V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Catalyzes the reversible oxidation of malate to
CC oxaloacetate (By similarity).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -1- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ENBL; AB009456; AAL51319.1; ALT_INIT; Genomic_DNA.
DR PIR; AD3269; AD3269.
DR HSSP; P80040; 1GUY.
DR HAMAP; MF 00487; -; 1. LDH_MDH.
DR InterPro; IPR001557; 1. LDH_MDH.
DR InterPro; IPR001236; 1dh.
DR InterPro; IPR011275; MalatedH_bact.
DR InterPro; IPR001252; Mdh_AS.
DR PANTHER; PTHR11540; 1dh; 1.
DR Pfam; PF02866; Ldh_1_C; 1.
DR Pfam; PF00056; Ldh_1_N; 1.
DR PIRSF; PIRSF000102; Ldh_mal_DH; 1.
DR PRINTS; PR00086; LLDHDSGNASE.
DR TIGRFAMs; TIGR01763; MalatedH_bact; 1.
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.
FT ACT_SITE 149 149 Proton relay (By similarity).
FT ACT_SITE 176 176 Proton relay (By similarity).
FT BINDING 83 83 Substrate carboxyl (By similarity).
FT BINDING 89 89 Substrate carboxyl (By similarity).
FT BINDING 152 152 Substrate carboxyl (By similarity).
SQ SEQUENCE 320 AA; 33666 MW; FD73DD8A3654AFB2 CRC64;

Query Match 51.9%; Score 876.5; DB 1; Length 320;
Best Local Similarity 54.2%; Pred. No. 3.4e-58;
Matches 174; Conservative 53; Mismatches 89; Indels 5; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSRLGDLVFLFDVVPNPMGMKAMDISHNSVVDGTITVG 68
DB 3 RKKIALGSGMIGTMAFLCSRLGDLVFLFDVVPNPMGMKAMDISHNSVVDGTITVG 62
QY 69 SNSYECLKADVVIITAGITKIPGSKDKEWSRMDLLFPVNIKIMREYGAAIKSYCPNAFVI 128
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Db 63 ANDYAAIEGADVIVTAGVPRKPG-----MSRDDLLGLNLKVMQVQAGIKKYAPEAFVI 117
Qy 129 NITNPLDVMVAALQESSGLPHRRICGMAGMLDSSRRFRMIADKLEVSPPRVQGVGVH 189
Db 118 CITNPLDAMWALQKFSGLPAHKVGVGMAGVLDLSARFRYFLSEEFNSVEDVTAFLVGGH 177
Qy 189 DHMVPLSRVATVNGIPLSEFVKKWKIKOBEVDVIVOKTKVAGGIVRLGGSAYYAPGA 248
Db 178 DSMVPLARYSTVAGIPLSLDLVKMGWTSODKLDKIIOQRDGGAEIVGLLTKGSAFYAPAA 237
Qy 249 SAIQMAESYLKDKRVRVMVSCYLOGQGVQVNHVGLVPCVIGGRGVKEIIIELELTAQBRQE 308
Db 238 SAIQMAESYLKDKRVRVPAALQSSQGVKMDYGVVPTVIGANGVERIIIDLDKDEKAQ 297
Qy 309 LQGSIDEVKEKQIAALDAS 329
Db 298 FDKSVASVAGLCEACIGIAPS 318

RESULT 12
ID MDH_AGRTS STANDARD; PRT; 320 AA.
AC 07CWK7; 08UC59;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37).
GN Name=mdh; OrderedLocusNames=Atu2639, AGR C 4782;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Agrobacterium.
-OR NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21608551; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Sebubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
OKura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saepthammachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58."
RL Science 294:2317-2323 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Ourolo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
CC -1- FUNCTION: Catalyzes the reversible oxidation of malate to
oxaloacetate (By similarity).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -1- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AE009211; AAL43620.1; -, Genomic DNA.
CC EMBL; AE008177; AAK88360.1; ALT_INIT; Genomic DNA.

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DR PIR; AF2900; AF2900.
DR PIR; G97675; G97675.
DR HSSP; P80040; IGUY.
DR HAMAP; MF 00487; -, 1.
DR InterPro; IPR001557; L_LDH_MDH.
DR InterPro; IPR001236; Ldh.
DR InterPro; IPR011275; MalateDH_bact.
DR InterPro; IPR001252; Mdh_AS.
DR PANTHER; PTHR11540; Ldh; 1.
DR Pfam; PF02866; Ldh_1_C; 1.
DR Pfam; PF00056; Ldh_1_N; 1.
DR PIRSF; PIRSF000102; Lac_mal_DH; 1.
DR PRINTS; PRO0086; LLDHDEGNASE.
DR TIGRFAWS; TIGR01763; MalateDH_bact; 1.
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.
FT ACT_SITE 149 176 176 proton relay (By similarity).
FT BINDING 83 83 Substrate carboxyl (By similarity).
FT BINDING 89 89 Substrate carboxyl (By similarity).
FT BINDING 152 152 Substrate carboxyl (By similarity).
SQ SEQUENCE 320 AA; 33537 MW; 3073A7C3BC0FC5E CRC64;

Query Match 51.7%; Score 873.5; DB 1; Length 320;
Best Local Similarity 53.2%; Pred No. 5.7e-58;
Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSLRELGDVVLDFVVPNPMGKAMDISHNSVVDPTGVY 68
Db 3 RKKIALIGSGMIGTTLAHLASLAKELGDIVLFDIADGIPQKGLDIAQSGPVEGFNAKLSG 62
Qy 69 SNSYECLKGADVIVITAGITKIPKSDKEKSRMDLLPVNIKIMREVCAAIKSYCPNAPVI 128
Db 63 ASDYAAIEGADVIVTAGVPRKPG-----MSRDDLLGLNLKVMQVQAGIKKYAPEAFVI 117
Qy 129 NITNPLDVMVAALQESSGLPHRRICGMAGMLDSSRRFRMIADKLEVSPPRVQGVGVH 188
Db 118 CITNPLDAMWALQKFSGLPKNVGMAGVLDLSARFRYFLSEEFNSVEDVTAFLVGGH 177
Qy 189 DHMVPLSRVATVNGIPLSEFVKKWKIKOBEVDVIVOKTKVAGGIVRLGGSAYYAPGA 248
Db 178 DTMVPLARYSTVAGVPLTDLVKMGWLTAELEQIIOQRDGGAEIVGLLTKGSAFYAPAA 237
Qy 249 SAIQMAESYLKDKRVRVMVSCYLOGQGVQVNHVGLVPCVIGGRGVKEIIIELELTAQBRQE 308
Db 238 SAIQMAESYLKDKRVRVPAALQSSQGVKMDYGVVPTVIGANGVERIIIELELTAQBRQE 297
Qy 309 LQGSIDEVKEKQIA 322
Db 298 FDKSVASVAGLCEA 311

RESULT 13
MDH_RHIME STANDARD; PRT; 320 AA.
ID MDH_RHIME STANDARD; PRT; 320 AA.
AC Q9EYJ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37).
GN Name=mdh; OrderedLocusNames=R03056; ORFNames=SMC02479;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dymov S.I., Meek D.J., Driscoll B.T.;
RT "Isolation of a malate dehydrogenase mutant and genes encoding a
RT putative TCA cycle operon of Sinorhizobium meliloti."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=1021;

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RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler P., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Maeyu U.,
RA Pohl T., Portetelie D., Pueher A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -!- FUNCTION: Catalyzes the reversible oxidation of malate to
CC oxaloacetate (By similarity).
CC -!- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -!- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF322647; AAC41996.1; -; Genomic_DNA.
DR EMBL; AL591792; CAC47635.1; -; Genomic_DNA.
DR HSSP; P80040; IGUY.
DR HAMAP; MF 00487; -; 1.
DR InterPro; IPR001557; L_LDH_MDH.
DR InterPro; IPR001236; LDh.
DR InterPro; IPR011275; MalatedDH_bact.
DR InterPro; IPR001252; Mdh_AS.
DR PANTHER; PTHR11540; ldh; 1.
DR Pfam; PF02866; Ldh_1_C; 1.
DR Pfam; PF00056; Ldh_1_N; 1.
DR PIRSF; PIRSF000102; Lac_mal_DH; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR TIGRFAMs; TIGR01763; MalatedDH_bact; 1.
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.
FT ACT SITE 149 176 Proton relay (By similarity).
FT ACT SITE 176 176 Proton relay (By similarity).
FT BINDING 83 83 Substrate carboxyl (By similarity).
FT BINDING 89 89 Substrate carboxyl (By similarity).
FT BINDING 152 152 Substrate carboxyl (By similarity).
SQ SEQUENCE 320 AA; 33611 MW; 3CF1514C7211F9FA CRC64;

Query Match 51.7%; Score 873.5; DB 1; Length 320;
Best Local Similarity 53.2%; Pred. No. 5.7e-58;
Matches 167; Conservative 63; Mismatches 79; Indels 5; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSRELGDVVLFDVVPNPMGKAMDISHNSVVDITGVG 68
Db 3 RNKIALIGSGMIGTTLAHLAAGLKGELGDLVLDIADGIPQGLDIAQSSPVEGFDASLTG 62

QY 69 SNSYECLKADVVIIITAGITKIPGKSDKESRMDLLPVNIKREVGAAIKSCPNAFVI 128
Db 63 ASDYSIAEGADVCIIVTAGVPRKPG-----MSRDDLLGINLKVMQEQGAGIKKYAPNAPVI 117

QY 129 NITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEYSRDRVQGVIGVHG 188
Db 118 CITNPLDAMVWALQKFSGLPKNVGVAGVLDSSRFLFLAEFNVSVKDIATFVLGGHG 177

QY 189 DHMVPLSRATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGIEVRLLLQGSAYYAPGA 248
Db 178 DTWVPLARYSTVAGIPLDILQMGWTTTKEKLDQIIQRTDGGAEIVGLLTKGSAYYAPAA 237

QY 249 SATQMAESYLKDKRVMVSCYLOGQGVQNHLYLQVPCVIGGRQVEKIELELTAEQRQE 308
Db 238 SAIEMAEAYLKDKRVLPCAAHLSSGGYGVKDMYVGVPTVIGAGGIERIIEIDLKGEKEA 297

QY 309 LOGSIDVEKEMOKA 322
Db 298 FDKSVAAVAGLCEA 311
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RESULT 14
MDH_BARQU

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ID MDH_BARQU STANDARD; PRT; 320 AA.
AC Q6FYD0;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37).
GN Names=mdh; OrderedLocusNames=BQ13450;
OS Bartonella quintana (Rochalimaea quintana).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=803;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Toulouse;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg B.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
CC -!- FUNCTION: Catalyzes the reversible oxidation of malate to
CC oxaloacetate (By similarity).
CC -!- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -!- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX897700; CAF26803.1; -; Genomic_DNA.
DR HAMAP; MF_00487; -; 1.
DR InterPro; IPR001088; Glyco_hydro_4.
DR InterPro; IPR001557; L_LDH_MDH.
DR InterPro; IPR001236; LDh.
DR InterPro; IPR011275; MalatedDH_bact.
DR InterPro; IPR001252; Mdh_AS.
DR PANTHER; PTHR11540; ldh; 1.
DR Pfam; PF02866; Ldh_1_C; 1.
DR Pfam; PF00056; Ldh_1_N; 1.
DR PIRSF; PIRSF000102; Lac_mal_DH; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR TIGRFAMs; TIGR01763; MalatedDH_bact; 1.
KW Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.
FT ACT SITE 149 176 Proton relay (By similarity).
FT ACT SITE 176 176 Proton relay (By similarity).
FT BINDING 83 83 Substrate carboxyl (By similarity).
FT BINDING 89 89 Substrate carboxyl (By similarity).
FT BINDING 152 152 Substrate carboxyl (By similarity).
SQ SEQUENCE 320 AA; 33935 MW; 5A8DB8A64348D544 CRC64;

Query Match 51.6%; Score 870.5; DB 1; Length 320;
Best Local Similarity 53.5%; Pred. No. 9.6e-58;
Matches 170; Conservative 62; Mismatches 81; Indels 5; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSRELGDVVLFDVVPNPMGKAMDISHNSVVDITGVG 68
Db 3 RNKIALIGSGMIGTTLAHLAAGLKGELGDLVLDIADGIPQGLDIAQSSPVEGFDVSLTG 62

QY 69 SNSYECLKADVVIIITAGITKIPGKSDKESRMDLLPVNIKREVGAAIKSCPNAFVI 128
Db 63 ANYTEAIEGADVIVTAGVARKPG-----MSRDDLLGINLKVMQEQGAGIKKYASSAFVI 117

QY 129 NITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEYSRDRVQGVIGVHG 188
Db 118 CITNPLDAMVWALQKFSGLPKNVGVAGVLDSSRFLFLAEFNVSVKDIATFVLGGHG 177

QY 189 DHMVPLSRATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGIEVRLLLQGSAYYAPGA 248
Db 178 DSMVPLRVSTVGGISLPLVKMGWTTQEKIQIIQVRNGGAEIVGLLTKGSAYYAPAA 237
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| Qy | 249 | SAIQWAEASYLDRKRWVWCSCYLOQGYGVNHYLVGPCVIGRGVKEKIEELBTQERQE | 308 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 238 | SAISNAEAYLKDIKRWVPVATYLSGEYGVKDTYVGVVVLGAGGVVERVIEDLDKERSA | 297 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 309 | LOGSIDEVKEMOKAIAAL | 326 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 298 | FEQSNVAVKLCERACIAI | 315 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <p>RESULT 15</p> <p>MDH_BRUAB</p> <table border="0"> <tr> <td>ID</td><td>MDH_BRUAB</td><td>STANDARD;</td><td>PRT;</td><td>320 AA.</td></tr> <tr> <td>AC</td><td>Q57AX1:</td><td colspan="3"></td></tr> <tr> <td>DT</td><td>13-SEP-2005</td><td>(Rel. 48, Created)</td><td colspan="2"></td></tr> <tr> <td>DT</td><td>13-SEP-2005</td><td>(Rel. 48, Last sequence update)</td><td colspan="2"></td></tr> <tr> <td>DT</td><td>13-SEP-2005</td><td>(Rel. 48, Last annotation update)</td><td colspan="2"></td></tr> <tr> <td>DE</td><td>Malate dehydrogenase</td><td>(EC 1.1.1.37).</td><td colspan="2"></td></tr> <tr> <td>GN</td><td>Name=mdh; OrderedLocusNames=BruAbl_1903;</td><td colspan="3"></td></tr> <tr> <td>OS</td><td>Brucella abortus.</td><td colspan="3"></td></tr> <tr> <td>OC</td><td>Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;</td><td colspan="3"></td></tr> <tr> <td>OC</td><td>Brucellaceae; Brucella.</td><td colspan="3"></td></tr> <tr> <td>OX</td><td>NCBI_TaxID=235;</td><td colspan="3"></td></tr> <tr> <td>OX</td><td>{1}</td><td colspan="3"></td></tr> <tr> <td>RP</td><td>NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].</td><td colspan="3"></td></tr> <tr> <td>RP</td><td>STRAIN=9-941 / Biovar 1;</td><td colspan="3"></td></tr> <tr> <td>RC</td><td>PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;</td><td colspan="3"></td></tr> <tr> <td>RA</td><td>Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,</td><td colspan="3"></td></tr> <tr> <td>RA</td><td>Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;</td><td colspan="3"></td></tr> <tr> <td>RT</td><td>"Completion of the genome sequence of Brucella abortus and comparison</td><td colspan="3"></td></tr> <tr> <td>RT</td><td>to the highly similar genomes of Brucella melitensis and Brucella</td><td colspan="3"></td></tr> <tr> <td>RT</td><td>suis.";</td><td colspan="3"></td></tr> <tr> <td>RL</td><td>J. Bacteriol. 187:2715-2726(2005).</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>-1- FUNCTION: Catalyzes the reversible oxidation of malate to</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>oxaloacetate (By similarity).</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>-1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>-1- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family.</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>-1- This Swiss-Prot entry is copyright. It is produced through a collaboration</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>between the Swiss Institute of Bioinformatics and the EMBL outstation</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>the European Bioinformatics Institute. There are no restrictions on its</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>use as long as its content is in no way modified and this statement is not</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>removed.</td><td colspan="3"></td></tr> <tr> <td>CC</td><td>EMBL: AE017223; AAX75213.1; -; Genomic_DNA.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>HMAP; MF_00487; -; 1_LDH_MDH.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>InterPro; IPR001557; 1_LDH_MDH.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>InterPro; IPR001236; ldh.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>InterPro; IPR011275; MalatedH_bact.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>PANTHER; PTHR11540; ldh; 1.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>Pfam; PF02866; Ldh_1_C; 1.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>Pfam; PF00056; Ldh_1_N; 1.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>PIRSF; PIRSF000102; Lac_mal_DH; 1.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>PRINTS; PR00086; LLDHDRGNASE.</td><td colspan="3"></td></tr> <tr> <td>DR</td><td>TIGRFAMs; TIGR01763; MalatedH_bact; 1.</td><td colspan="3"></td></tr> <tr> <td>KW</td><td>Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle.</td><td colspan="3"></td></tr> <tr> <td>FT</td><td>ACT_SITE 149 149</td><td colspan="3">Proton relay (By similarity).</td></tr> <tr> <td>FT</td><td>ACT_SITE 176 176</td><td colspan="3">Proton relay (By similarity).</td></tr> <tr> <td>FT</td><td>BINDING 83 83</td><td colspan="3">Substrate carboxyl (By similarity).</td></tr> <tr> <td>FT</td><td>BINDING 89 89</td><td colspan="3">Substrate carboxyl (By similarity).</td></tr> <tr> <td>FT</td><td>BINDING 152 152</td><td colspan="3">Substrate carboxyl (By similarity).</td></tr> <tr> <td>SC</td><td>SEQUENCE 320 AA; 33704 MW; C212BA88F0241677 CRC64;</td><td colspan="3"></td></tr> <tr> <td colspan="4"> <p>Query Match 51.5%; Score 868.5; DB 1; Length 320;</p> <p>Best Local Similarity 53.9%; Pred. No. 1.4e-57;</p> <p>Matches 173; Conservative 53; Mismatches 90; Indels 5; Gaps 1</p> </td></tr> <tr> <td>Qy</td><td>9</td><td>RPKIAMVSGMIGGTMAFLCSIRLRELDGVVLPDVPNPMWGMKAMDSHNSVVDTGITVYG</td><td>68</td></tr> <tr> <td>Db</td><td>3</td><td>RNKALIGSGMIGGTLAHLAGLKGELGDVVLFDIAEGTQGGKGLDIAESSVDGPAKFTG</td><td>62</td></tr> <tr> <td>Qy</td><td>69</td><td>SNSYECLKGADVITITAGITIKIPGKSDEKWSRMDLLPVNIMREVGAIAKSYCPNAPVI</td><td>128</td></tr> </table> | | | | ID | MDH_BRUAB | STANDARD; | PRT; | 320 AA. | AC | Q57AX1: | | | | DT | 13-SEP-2005 | (Rel. 48, Created) | | | DT | 13-SEP-2005 | (Rel. 48, Last sequence update) | | | DT | 13-SEP-2005 | (Rel. 48, Last annotation update) | | | DE | Malate dehydrogenase | (EC 1.1.1.37). | | | GN | Name=mdh; OrderedLocusNames=BruAbl_1903; | | | | OS | Brucella abortus. | | | | OC | Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; | | | | OC | Brucellaceae; Brucella. | | | | OX | NCBI_TaxID=235; | | | | OX | {1} | | | | RP | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. | | | | RP | STRAIN=9-941 / Biovar 1; | | | | RC | PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005; | | | | RA | Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L., | | | | RA | Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.; | | | | RT | "Completion of the genome sequence of Brucella abortus and comparison | | | | RT | to the highly similar genomes of Brucella melitensis and Brucella | | | | RT | suis."; | | | | RL | J. Bacteriol. 187:2715-2726(2005). | | | | CC | -1- FUNCTION: Catalyzes the reversible oxidation of malate to | | | | CC | oxaloacetate (By similarity). | | | | CC | -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH. | | | | CC | -1- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family. | | | | CC | -1- This Swiss-Prot entry is copyright. It is produced through a collaboration | | | | CC | between the Swiss Institute of Bioinformatics and the EMBL outstation | | | | CC | the European Bioinformatics Institute. There are no restrictions on its | | | | CC | use as long as its content is in no way modified and this statement is not | | | | CC | removed. | | | | CC | EMBL: AE017223; AAX75213.1; -; Genomic_DNA. | | | | DR | HMAP; MF_00487; -; 1_LDH_MDH. | | | | DR | InterPro; IPR001557; 1_LDH_MDH. | | | | DR | InterPro; IPR001236; ldh. | | | | DR | InterPro; IPR011275; MalatedH_bact. | | | | DR | PANTHER; PTHR11540; ldh; 1. | | | | DR | Pfam; PF02866; Ldh_1_C; 1. | | | | DR | Pfam; PF00056; Ldh_1_N; 1. | | | | DR | PIRSF; PIRSF000102; Lac_mal_DH; 1. | | | | DR | PRINTS; PR00086; LLDHDRGNASE. | | | | DR | TIGRFAMs; TIGR01763; MalatedH_bact; 1. | | | | KW | Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle. | | | | FT | ACT_SITE 149 149 | Proton relay (By similarity). | | | FT | ACT_SITE 176 176 | Proton relay (By similarity). | | | FT | BINDING 83 83 | Substrate carboxyl (By similarity). | | | FT | BINDING 89 89 | Substrate carboxyl (By similarity). | | | FT | BINDING 152 152 | Substrate carboxyl (By similarity). | | | SC | SEQUENCE 320 AA; 33704 MW; C212BA88F0241677 CRC64; | | | | <p>Query Match 51.5%; Score 868.5; DB 1; Length 320;</p> <p>Best Local Similarity 53.9%; Pred. No. 1.4e-57;</p> <p>Matches 173; Conservative 53; Mismatches 90; Indels 5; Gaps 1</p> | | | | Qy | 9 | RPKIAMVSGMIGGTMAFLCSIRLRELDGVVLPDVPNPMWGMKAMDSHNSVVDTGITVYG | 68 | Db | 3 | RNKALIGSGMIGGTLAHLAGLKGELGDVVLFDIAEGTQGGKGLDIAESSVDGPAKFTG | 62 | Qy | 69 | SNSYECLKGADVITITAGITIKIPGKSDEKWSRMDLLPVNIMREVGAIAKSYCPNAPVI | 128 |
| ID | MDH_BRUAB | STANDARD; | PRT; | 320 AA. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| AC | Q57AX1: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DT | 13-SEP-2005 | (Rel. 48, Created) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DT | 13-SEP-2005 | (Rel. 48, Last sequence update) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DT | 13-SEP-2005 | (Rel. 48, Last annotation update) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DE | Malate dehydrogenase | (EC 1.1.1.37). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| GN | Name=mdh; OrderedLocusNames=BruAbl_1903; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| OS | Brucella abortus. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| OC | Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| OC | Brucellaceae; Brucella. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| OX | NCBI_TaxID=235; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| OX | {1} | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RP | STRAIN=9-941 / Biovar 1; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RC | PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RA | Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L., | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RA | Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RT | "Completion of the genome sequence of Brucella abortus and comparison | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RT | to the highly similar genomes of Brucella melitensis and Brucella | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RT | suis."; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RL | J. Bacteriol. 187:2715-2726(2005). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | -1- FUNCTION: Catalyzes the reversible oxidation of malate to | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | oxaloacetate (By similarity). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | -1- SIMILARITY: Belongs to the LDH/MDH superfamily. MDH type 3 family. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | -1- This Swiss-Prot entry is copyright. It is produced through a collaboration | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | the European Bioinformatics Institute. There are no restrictions on its | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | use as long as its content is in no way modified and this statement is not | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | removed. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| CC | EMBL: AE017223; AAX75213.1; -; Genomic_DNA. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | HMAP; MF_00487; -; 1_LDH_MDH. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | InterPro; IPR001557; 1_LDH_MDH. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | InterPro; IPR001236; ldh. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | InterPro; IPR011275; MalatedH_bact. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | PANTHER; PTHR11540; ldh; 1. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | Pfam; PF02866; Ldh_1_C; 1. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | Pfam; PF00056; Ldh_1_N; 1. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | PIRSF; PIRSF000102; Lac_mal_DH; 1. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | PRINTS; PR00086; LLDHDRGNASE. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| DR | TIGRFAMs; TIGR01763; MalatedH_bact; 1. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| KW | Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid cycle. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| FT | ACT_SITE 149 149 | Proton relay (By similarity). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| FT | ACT_SITE 176 176 | Proton relay (By similarity). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| FT | BINDING 83 83 | Substrate carboxyl (By similarity). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| FT | BINDING 89 89 | Substrate carboxyl (By similarity). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| FT | BINDING 152 152 | Substrate carboxyl (By similarity). | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| SC | SEQUENCE 320 AA; 33704 MW; C212BA88F0241677 CRC64; | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <p>Query Match 51.5%; Score 868.5; DB 1; Length 320;</p> <p>Best Local Similarity 53.9%; Pred. No. 1.4e-57;</p> <p>Matches 173; Conservative 53; Mismatches 90; Indels 5; Gaps 1</p> | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 9 | RPKIAMVSGMIGGTMAFLCSIRLRELDGVVLPDVPNPMWGMKAMDSHNSVVDTGITVYG | 68 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 3 | RNKALIGSGMIGGTLAHLAGLKGELGDVVLFDIAEGTQGGKGLDIAESSVDGPAKFTG | 62 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 69 | SNSYECLKGADVITITAGITIKIPGKSDEKWSRMDLLPVNIMREVGAIAKSYCPNAPVI | 128 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

THIS PAGE BLANK (uspto)

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|--------|--------------------|
| | Score | Match | Length | | | |
| 1 | 876.5 | 51.9 | 326 | 2 | AD3269 | malate dehydrogena |
| 2 | 873.5 | 51.7 | 320 | 2 | AF2900 | malate dehydrogena |
| 3 | 873.5 | 51.7 | 352 | 2 | G97675 | malate dehydrogena |
| 4 | 830.5 | 50.4 | 320 | 2 | E87702 | malate dehydrogena |
| 5 | 837.5 | 49.6 | 314 | 2 | H97764 | malate dehydrogena |
| 6 | 826.5 | 49.0 | 314 | 2 | A71695 | malate dehydrogena |
| 7 | 740 | 43.8 | 312 | 2 | I40383 | malate dehydrogena |
| 8 | 729 | 43.2 | 312 | 2 | S61213 | malate dehydrogena |
| 9 | 709 | 42.0 | 314 | 2 | F84044 | malate dehydrogena |
| 10 | 634 | 37.6 | 324 | 2 | S75735 | probable malate de |
| 11 | 605.5 | 35.9 | 335 | 2 | E70453 | malate dehydrogena |
| 12 | 569 | 33.7 | 334 | 2 | D70444 | malate dehydrogena |
| 13 | 566.5 | 33.6 | 284 | 2 | AC2346 | malate dehydrogena |
| 14 | 560.5 | 33.2 | 313 | 2 | E72655 | probable malate de |
| 15 | 478 | 28.3 | 314 | 2 | H86671 | L-lactate dehydrog |
| 16 | 465.5 | 27.6 | 313 | 2 | AC1463 | L-lactate dehydrog |
| 17 | 463.5 | 27.5 | 313 | 2 | AC1101 | L-lactate dehydrog |
| 18 | 460 | 27.3 | 321 | 2 | E96649 | L-lactate dehydrog |
| 19 | 455 | 27.0 | 318 | 1 | DEBSLM | L-lactate dehydrog |
| 20 | 454 | 26.9 | 313 | 2 | E96932 | L-lactate dehydrog |
| 21 | 440.5 | 26.1 | 353 | 2 | F71441 | L-lactate dehydrog |
| 22 | 440 | 26.1 | 318 | 2 | S08182 | L-lactate dehydrog |
| 23 | 439.5 | 26.0 | 319 | 2 | S36863 | L-lactate dehydrog |
| 24 | 434.5 | 25.7 | 312 | 2 | H64250 | L-lactate dehydrog |
| 25 | 431.5 | 25.6 | 326 | 1 | DEBLA | L-lactate dehydrog |
| 26 | 431 | 25.5 | 319 | 2 | S08183 | L-lactate dehydrog |
| 27 | 428 | 25.4 | 317 | 2 | B29704 | L-lactate dehydrog |
| 28 | 424.5 | 25.1 | 317 | 2 | S00019 | L-lactate dehydrog |
| 29 | 423.5 | 25.1 | 320 | 2 | JQ0183 | L-lactate dehydrog |

```
RESULT 2
AF2300
malate dehydrogenase mdh [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2900
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, F.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-320 <R>
A;Cross-references: UNIPROT:Q8UC59; UNIPARC:UPI000016474B; GB:AE008688; PIDN:AA443620.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: mdh
A;Map position: circular chromosome
C;Superfamily: L-lactate dehydrogenase

Query Match 51.7%; Score 873.5; DB 2; Length 320;
Best Local Similarity 53.2%; Pred. No. 1.3e-59;
Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSRLGDLVFLFDVVPNPMGKAMDISHNSSVVDGTITVYG 68
Db 3 RKXIALIGSGMIGTMAFLCSRLGDLVFLFDIADGIPQKGLDIAQSGPVEGFNAKLSG 62

Qy 69 SNSYECLKGADVVIITAGITKIPKSKDKWSRMDLLPVNIKIMREVGAAIKSCYCPNAFVI 128
Db 63 ASDYAAIEGADVCIIVTAGVARKPG-----MSRDDLLGINKVMEQVGAGIKKYAPNAFVI 117

Qy 129 NITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDQVMGVGHG 198
Db 118 CITNPLDAMVWALQKFSGLPKNKVGMAGVLDARSARFLFLAEFNVSVQDVTAFVLGGHG 177

Qy 189 DHMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGQGSAYTAPGA 248
Db 178 DTMVPLARYSTVGGVPLTDLVKGWLTAELEQIIQTRDGGAEIVGLLKTGSAYTAPAA 237

Qy 249 SAIQMAESYLKDKRVMVCSYLGQGYQVQNHVYLGVPVCGVGRGVEKIIIELELTAQERQE 308
Db 238 SAIQMAESYLKDKRVLPAHAHLSGGYGVDDMTVGVPTIIGAGGIERVIEELNKEEAA 297

Qy 309 LQGSIDEVEMQKA 322
Db 298 FQKSVGAVAGLCEA 311

RESULT 3
G97675
malate dehydrogenase [imported] - Agrobacterium tumefaciens (strain C58, Cerson)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97675
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <R>
A;Cross-references: UNIPROT:Q8UC59; UNIPARC:UPI000000D1F8D; GB:AE007869; PIDN:AAK88360.1;
C;Genetics:
A;Gene: AGR_C_4782
A;Map position: circular chromosome
```

C;Superfamily: L-lactate dehydrogenase

```
Query Match 51.7%; Score 873.5; DB 2; Length 352;
Best Local Similarity 53.2%; Pred. No. 1.5e-59;
Matches 167; Conservative 60; Mismatches 82; Indels 5; Gaps 1;

Qy 9 RPKIAMVSGMIGTMAFLCSRLGDLVFLFDVVPNPMGKAMDISHNSSVVDGTITVYG 68
Db 35 RKXIALIGSGMIGTMAFLCSRLGDLVFLFDIADGIPQKGLDIAQSGPVEGFNAKLSG 94

Qy 69 SNSYECLKGADVVIITAGITKIPKSKDKWSRMDLLPVNIKIMREVGAAIKSCYCPNAFVI 128
Db 95 ASDYAAIEGADVCIIVTAGVARKPG-----MSRDDLLGINKVMEQVGAGIKKYAPNAFVI 149

Qy 129 NITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDQVMGVGHG 198
Db 150 CITNPLDAMVWALQKFSGLPKNKVGMAGVLDARSARFLFLAEFNVSVQDVTAFVLGGHG 209

Qy 189 DHMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGQGSAYTAPGA 248
Db 210 DTMVPLARYSTVGGVPLTDLVKGWLTAELEQIIQTRDGGAEIVGLLKTGSAYTAPAA 269

Qy 249 SAIQMAESYLKDKRVMVCSYLGQGYQVQNHVYLGVPVCGVGRGVEKIIIELELTAQERQE 308
Db 270 SAIQMAESYLKDKRVLPAHAHLSGGYGVDDMTVGVPTIIGAGGIERVIEELNKEEAA 329

Qy 309 LQGSIDEVEMQKA 322
Db 330 FQKSVGAVAGLCEA 343
```

RESULT 4

E87702

malate dehydrogenase [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: E87702

R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eieen, J.; Heidelberg, J.

n, J.; Laub, M.R.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: E87702

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-320 <STO>

A;Cross-references: UNIPROT:Q9A2B1; UNIPARC:UPI00000C7B5D; GB:AE005673; NID:g13425411; PJ

C;Genetics:

A;Gene: CC3655

C;Superfamily: L-lactate dehydrogenase

```
Query Match 50.4%; Score 850.5; DB 2; Length 320;
Best Local Similarity 51.1%; Pred. No. 7.7e-58;
Matches 164; Conservative 60; Mismatches 92; Indels 5; Gaps 1;
```

```
Qy 9 RPKIAMVSGMIGTMAFLCSRLGDLVFLFDVVPNPMGKAMDISHNSSVVDGTITVYG 68
Db 3 RAKIALIGAMIGGTMAHAAAREELGDVILFDIAEGTPQKGLDIAEASAVFGKDVALKG 62

Qy 69 SNSYECLKGADVVIITAGITKIPKSKDKWSRMDLLPVNIKIMREVGAAIKSCYCPNAFVI 128
Db 63 ANDYADGADVCIIVTAGVPRKPG-----MSRDDLLGINKVMEQVGAGIKKYAPNAFVI 117

Qy 129 NITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPRDQVMGVGHG 198
Db 118 CITNPLDAMVWALQKFSGLPKNKVGMAGVLDARSARFAYFLAEATGVSVEDIHAHTLGGHG 177

Qy 189 DHMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIVQKTKVAGGEIVRLLGQGSAYTAPGA 248
Db 178 DMVPMVRHSTVGGGLPLPLVLKQWLSQDKLDAIVERTRKGGGEIVALLKTKGSFAFAPAE 237

Qy 249 SAIQMAESYLKDKRVMVCSYLGQGYQVQNHVYLGVPVCGVGRGVEKIIIELELTAQERQE 308
```

```
Db 238 SAATMATSYLKDKRVPCHATYLTGQGLNDLYGVVPVWVGAGAEKIVFETNDEKAM 297
Qy 309 LOGSIDEVKEMQKAI AALDAS 329
Db 298 FAKSVESVKGLMEACKAIDSS 318

RESULT 5
H97764
malate dehydrogenase (EC 1.1.1.37) [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: H97764
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rickettsia Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:2142074; PMID:11557893
A:Accession: H97764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <KUR>
A:Cross-references: UNIPROT:Q921A0; UNIPARC:UPI000012BE50; GB:AE006914; PIDN:AAL03058.1;
C:Gene: mdh
C:Superfamily: L-lactate dehydrogenase
C:Keywords: oxidoreductase

Query Match 49.68; Score 837.5; DB 2; Length 314;
Best Local Similarity 49.8%; Pred. No. 7.5e-57;
Matches 156; Conservative 72; Mismatches 80; Indels 5; Gaps 1;

Qy 11 KIAMVSGMIGTGMFLCSRLRELDVDFVVPNMPMGKAMDISHNSVVDVTGTVVGSN 70
Db 6 KISLIGSGNIGTGLAHLSISRLKGLDIVLFDVTEGVPGKALDLMQAGTIGSDIKIKGTN 65
Qy 71 SYECLGADVVIITAGITKTPGSKDKSWMDLLPVNKKIMREVGAAIKSYCNPAFVNI 130
Db 66 DYKDIEGSDAIIITAGLPRKPG-----MSREDLISINTGIMKTVAANKVYAPDAFVIV 120
Qy 131 TNPDLVMAALQESSGLPHHRI CGMAGMLDSSRRFRMIADKLEVPDVGWIGVHGHDH 190
Db 121 TNPDLVMAVYMLKESGLPHNKGVLGAGVLDSSRNFLAEKFKSVNVMNSMVLGGHGDA 180
Qy 191 MVPLSRVATNGIPLSEFVKKGWIKQBEVDIVQKTKVAGGEIVRLLGQGSAYYAPGASA 250
Db 181 MVPLARYSTISGVPIPLIKWGLSSNENIEKIDRTNGGGEIVALLKTSAYYAPASA 240
Qy 251 IQMAESYLKDKRKMVWCSCYLGQGYQVONHYLGVPCVIGRGVEKIIIELELTAEQRELQ 310
Db 241 IEMLESYLKDKRQILTCAAHLQGEYGVHDLVGVPIIMIGKGVLRVIELQLTAEKALFD 300
Qy 311 GSIDEVKEMQKAI 323
Db 301 KSVGEVKKLIETI 313

RESULT 6
A71695
malate dehydrogenase (mdh) RP376 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: A71695
R:Andersson, S.G.E.; Zonorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: A71695
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-314 <AND>
A:Cross-references: UNIPROT:Q92DF3; UNIPARC:UPI000012BE51; GB:AJ235271; GB:AJ235269; NID:
A:Experimental source: strain Madrid E
```

```
C:Genetics:
C:Gene: mdh; RP376
C:Superfamily: L-lactate dehydrogenase

Query Match 49.0%; Score 826.5; DB 2; Length 314;
Best Local Similarity 49.8%; Pred. No. 5.3e-56;
Matches 157; Conservative 70; Mismatches 81; Indels 7; Gaps 2;

Qy 5 EKVRPKIAMVSGMIGTGMFLCSRLRELDVDFVVPNMPMGKAMDISHNSVVDVTGI 64
Db 2 KKN--PKISLIGSGNIGTGLAHLSISRLKGLDIVLFDVTEGVPGKALDLMQAAATIEGSDI 59
Qy 65 TVYGSNSYECLGADVVIITAGITKTPGSKDKSWMDLLPVNKKIMREVGAAIKSYCN 124
Db 60 KIKGTNDYRDIEGSDAIIITAGLPRKPG-----MSRDDLSISVNTKMKOVAQNIKYAQN 114
Qy 125 AFVINITNPDLVMAALQESSGLPHHRI CGMAGMLDSSRRFRMIADKLEVPDVGWIMVI 184
Db 115 AFVIVITNPDLVMAVYMLKESGLPHNKGVLGAGVLDSSRNFLAEKFKSVNVMNSIVL 174
Qy 185 GVHGDHMPVLSRYATNGIPLSEFVKKGWIKQBEVDIVQKTKVAGGEIVRLLGQGSAYY 244
Db 175 GGHGDTMVPPLRYSTISGVPIPLIKWGLSSNENIEKIDRTNGGGEIVKLLKTSAYY 234
Qy 245 APCASAIQMAESYLKDKRKMVWCSCYLGQGYQVONHYLGVPCVIGRGVEKIIIELELT 304
Db 235 APAASAIAMLESYLKDKRQILTCAAHLQGEYGVHDLVGVPIIMIGKGVLRVIELQUTE 294
Qy 305 ERQELQGSIDEVKEM 319
Db 295 EKILFYKSVTEVKKL 309

RESULT 7
I40383
malate dehydrogenase (EC 1.1.1.37) citH - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40383; B69600
R:Jin, S.; Sonenshein, A.L.
J. Bacteriol. 176, 4669-4679, 1994
A:Title: Identification of two distinct Bacillus subtilis citrate synthase genes.
A:Reference number: I40379; MUID:94321340; PMID:8045898
A:Accession: I40383
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-312 <RES>
A:Cross-references: UNIPROT:P49814; UNIPARC:UPI00000608B9; EMBL:U05257; NID:g1045295; PII
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec
C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabbret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69600
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-312 <KUN>
A:Cross-references: UNIPARC:UPI00000608B9; GB:Z99118; GB:AL009136; NID:g2635200; PIDN:CA
A:Experimental source: strain 168
C:Genetics:
C:Gene: citH
C:Superfamily: L-lactate dehydrogenase
```


A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-Fixing Cyanobacterium And
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AC2346
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-284 <KUR>
A;Cross-references: UNIPROT:Q8YF78; UNIPARC:UPI000000CEABC; GB:BA000019; PIDN:BAB76021.1;
A;Experimental source: strain PCC 7120
C;Genetics:
C;Gene: alr4322
C;Superfamily: L-lactate dehydrogenase

Query Match 33.6%; Score 566.5; DB 2; Length 284;
Best Local Similarity 42.0%; Pred. No. 4.4e-36;
Matches 124; Conservative 54; Mismatches 90; Indels 27; Gaps 5;

QY 36 VVLFDVVPNNPMGKAMD I-----SHNSVVDTGTVVGSNYECLKGADVVIITAGIT 88
DB 1 MVLLDVEGIFQGLALLDLLEARGIELHNRQII-----GTNNVADTSGSQIVVITAGFP 53
QY 89 KIPGSKDESRMDLLPVNIKIMREVGAAIKSYCPNFAVINITNPLDMVVAALQESSGLP 148
DB 54 RKFG-----MSRDDLLRTNAKIVIEAKQAIAYSPYAIFIVTNPLDMVTYLAWEATGLP 108
QY 149 HHRICGMAGMLDSRFRMIADKLEVSPRDQGVIGVGHDMVPLSRVATVANGIPLSEF 208
DB 109 RNRMGMAGVLDGARFTFIALELGVLPADVKAMVGLSHGDLVWPLSRVATVANGIPIQL 168
QY 209 VKXGMIKQEBVDIVQKTVAGGEIVRLGQGSAYYAPGASAIQMAESYLKDRKRVNVC 268
DB 169 -----LDAVTIERLVERTRNGGAIEVELMTGGAFAPASATSLMVESILLNQSRLLPVS 223
QY 269 CYLQCGYGVNHYLGPVCVIGRGVEKIIIELETAQERQELQGSIDBVKEMQKAI 323
DB 224 IYLGQGYDLKDVVIGVPCRLGLNGIESVIELNLSDSEREALHS---AKSVQKNI 275

RESULT 14
E72655

probable malate dehydrogenase APE0672 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <KAW>
A;Cross-references: UNIPROT:Q9YEA1; UNIPARC:UPI000005DC3A; DDBJ:AP0000060; NID:95104188;
A;Experimental source: strain K1
C;Genetics:
C;Gene: APE0672
C;Superfamily: L-lactate dehydrogenase

Query Match 33.2%; Score 560.5; DB 2; Length 313;
Best Local Similarity 35.9%; Pred. No. 1.4e-35;
Matches 113; Conservative 72; Mismatches 119; Indels 11; Gaps 3;

QY 9 RPKIAMVSGMIGTMAFLCSRELGDVLFVDPVNNPMGKAMDISHNSVVDTGTVYG 68
DB 4 QPLITLIGAGKVGNGATVAMLMRMGRYDLDLLIARTPKPGQGEALDLAHAALGVDIRISG 63
QY 69 SNSVECLKGADVVIITAGITKIPGSKDESRMDLLPVNIKIMREVGAAIKSYCPNFAVI 128
DB 64 SNSVEDMRGSDIVLVITAGIKKPG-----MTRQLLEANANTWADLAEKIKAYAKDAIVV 118
QY 129 NITNPLDMVVAALQESSGLPHHRICGMAGMLDSRFRMIADKLEVSPRDQGVIGVGH 188
DB 119 ITTNPDAMTYVMYKKTGFFPRVIRGFSGLDSARMAYYISQKLGVSFKSVNAIVLGMHG 178

QY 189 DHMVPLSRVATVNGIPLSEFVKGMIKQEBVDIVQKTVAGGEIVRLGQGSAYVAPGA 248
DB 179 QKMFPVPRLUSSVGGVPLEHLSK-----BEIEVSETVNAGAKITELRGY-SSNYPAA 232
QY 249 SAIQMAESYLKDRKRVNVCSCYLQGYGVNHYLGPVCVIGRGVKEKIIIELELTAQERQ 308
DB 233 GLVLTVEAIKRSKRIYPYSLYLQGEYNDIVAEVPAVIGKSGIERIIEPLTEDEKRR 292
QY 309 LQGSIDBVKEMQKAI 323
DB 293 FDEAVQAVKLVETL 307

RESULT 15
H86671

L-lactate dehydrogenase (EC 1.1.1.27) [imported] - Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86671
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86671
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: UNIPROT:Q9CII4; UNIPARC:UPI000012E2D6; GB:AE005176; PID:gl2723247; P3
A;Experimental source: strain IL1403
C;Genetics:
C;Gene: ldhB
C;Superfamily: L-lactate dehydrogenase
C;Keywords: oxidoreductase

Query Match 28.3%; Score 478; DB 2; Length 314;
Best Local Similarity 32.8%; Pred. No. 3.1e-29;
Matches 105; Conservative 79; Mismatches 126; Indels 10; Gaps 5;

QY 6 KNTRPKIAMVSGMIGTMAFLCSRELGDVVLFDVVPNNPMGKAMDISHNSVVDTGI 64
DB 2 KITSRKVVIGTGVGTSTAYSMINQGLVNLVLIDVNDQKAEAGEALDLDGVSWGQENV 61
QY 65 TVYGSNSYECLKADVVIITAGITKIPGSKDESRMDLLPVNIKIMREVGAAIKSYCPN 124
DB 62 IVRAGDYKDC-KNADIVVVVTVAGVGNKPGQ-----SRDLVNTNAKIMRSIVTVQWDSGFD 115
QY 125 AFVINITNPLDMVVAALQESSGLPHHRICGMAGMLDSRFRMIADKLEVSPRDQGVMI 184
DB 116 GIFVIASNPVDILTYVAVWETSGLDQDSRIVGTGTTLDTFRKELATKLEIDPRSVHGYII 175
QY 185 GVHGDHMPLSRYATVNGIPLSEF-VKGMWIKQEBVDIVQKTVAGGEIVRLGQGSAY 243
DB 176 GEHGDSEVAVMSHTTVGGKPILEFIVKKNKIGVEDLSNLSNKVNAAYEIID--KKQATY 233
QY 244 YAPGASAIQMAESYLKDRKRVNVCSCYLQGYGVNHYLGPVCVIGRGVKEKIIIELELTA 303
DB 234 YGIGMSTARIVKAILNNEQAIFVSAYLGRGEYQGVFTGTVPISVNVQNGVREIIEINLIDA 293
QY 304 QERQELQGSIDBVKEMQKAI 323
DB 294 YEKQFEKSVSQLKEVIESI 313

Search completed: March 2, 2006, 19:40:42
Job time : 25 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:37:51 ; Search time 185 Seconds
(without alignments)
783.757 Million cell updates/sec

Title: US-09-390-846-2
Perfect score: 1688
Sequence: 1 MAVFEKTRPKIAVWGSMI.....GSIDEVKEMQKAAALDASK 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|---------------------|
| 1 | 1685 | 99.8 | 330 | 2 AAW11476 | AAW11476 Eimeria 1 |
| 2 | 880.5 | 52.2 | 320 | 8 ADS28805 | Ads28805 Bacterial |
| 3 | 873.5 | 51.7 | 319 | 8 ADS22408 | Ads22408 Bacterial |
| 4 | 873.5 | 51.7 | 320 | 8 ADS25456 | Ads25456 Bacterial |
| 5 | 873.5 | 51.7 | 320 | 8 ADS25841 | Ads25841 Bacterial |
| 6 | 862.5 | 51.1 | 311 | 8 ADS42318 | Ads42318 Bacterial |
| 7 | 862 | 51.1 | 322 | 8 ADS23027 | Ads23027 Bacterial |
| 8 | 850.5 | 50.4 | 320 | 8 ADS28046 | Ads28046 Bacterial |
| 9 | 848.5 | 50.3 | 320 | 8 ADN25360 | Adn25360 Bacterial |
| 10 | 847.5 | 50.2 | 320 | 8 ADS21490 | Ads21490 Bacterial |
| 11 | 828 | 49.1 | 315 | 2 AAR62605 | Aar62605 P. falcip |
| 12 | 828 | 49.1 | 315 | 2 AAY01690 | Aay01690 A. Plasmid |
| 13 | 740 | 43.8 | 312 | 8 ADS44807 | Ads44807 Bacterial |
| 14 | 709 | 42.0 | 314 | 8 ADS28362 | Ads28362 Bacterial |
| 15 | 706 | 41.8 | 329 | 2 AAR94013 | Aar94013 Heat resi |
| 16 | 697 | 41.3 | 312 | 8 ADS27485 | Ads27485 Bacterial |
| 17 | 694 | 41.1 | 289 | 9 ABM94287 | Abm94287 M. xanthu |
| 18 | 689 | 40.8 | 285 | 8 ADS30094 | Ads30094 Bacterial |
| 19 | 672 | 39.8 | 309 | 8 ADN26392 | Adn26392 Bacterial |
| 20 | 669.5 | 39.7 | 319 | 8 ADS24552 | Ads24552 Bacterial |
| 21 | 652.5 | 38.7 | 304 | 8 ADS21368 | Ads21368 Bacterial |
| 22 | 649.5 | 38.5 | 325 | 8 ADS23187 | Ads23187 Bacterial |
| 23 | 641 | 38.0 | 325 | 5 ABP40688 | Abp40688 Staphyloc |
| 24 | 641 | 38.0 | 325 | 8 ADS07962 | Ads07962 Staphyloc |

| | | | | | | |
|----|-------|------|-----|---|----------|-----------|
| 25 | 635 | 37.6 | 304 | 8 | ADS22139 | Bacterial |
| 26 | 635 | 37.6 | 317 | 8 | ADS30817 | Bacterial |
| 27 | 634 | 37.6 | 324 | 8 | ADN20169 | Bacterial |
| 28 | 628 | 37.2 | 299 | 8 | ADN27111 | Bacterial |
| 29 | 626.5 | 37.1 | 305 | 8 | ADS21934 | Bacterial |
| 30 | 625.5 | 37.1 | 309 | 8 | ADS29825 | Bacterial |
| 31 | 605.5 | 35.9 | 335 | 8 | ADN17485 | Bacterial |
| 32 | 569 | 33.7 | 334 | 8 | ADN17472 | Bacterial |
| 33 | 560.5 | 33.2 | 313 | 8 | ADS44426 | Bacterial |
| 34 | 529 | 31.3 | 197 | 8 | ADS25293 | Bacterial |
| 35 | 478 | 28.3 | 314 | 5 | ABBS3683 | Lactococc |
| 36 | 478 | 28.3 | 314 | 5 | ABBS3683 | Lactococc |
| 37 | 464 | 27.5 | 324 | 7 | ADC96859 | E. faeciu |
| 38 | 463.5 | 27.5 | 313 | 5 | ABBA7671 | Listeria |
| 39 | 462 | 27.4 | 312 | 8 | ADS27646 | Bacterial |
| 40 | 460 | 27.3 | 321 | 8 | ADOS9775 | B. subtil |
| 41 | 460 | 27.3 | 321 | 8 | ADS44643 | Bacterial |
| 42 | 458 | 27.1 | 312 | 8 | ADS27670 | Bacterial |
| 43 | 455 | 27.0 | 318 | 6 | ABR82282 | B. megate |
| 44 | 440.5 | 26.1 | 353 | 3 | AAG30183 | Arabidops |
| 45 | 439.5 | 26.0 | 319 | 8 | ADN20416 | Bacterial |

ALIGNMENTS

RESULT 1
AAW11476
ID AAW11476 standard; protein; 330 AA.

XX AC AAW11476;
XX DT 17-OCT-2003 (revised)
XX DT 29-APR-1997 (first entry)
XX DE Eimeria lactate dehydrogenase.
XX XX Lactate dehydrogenase; LDH; coccidiosis; vaccine; vector.
XX OS Eimeria acervulina; strain Houghton.
XX PN AU9656287-A.
XX PD 16-JAN-1997.
XX PF 02-JUL-1996; 96AU-00056287.
XX PR 03-JUL-1995; 95EP-00201801.
XX PA (ALKU) AKZO NOBEL NV.
XX PI Kok JJ, Van Den Boogaart P, Vermeulen AN;
XX DR WPI; 1997-109375/11.
XX DR N-PSDB; AAT51370.
XX PT Eimeria lactate dehydrogenase protein - used for prodn. of vaccines
XX PT against coccidiosis in poultry.
XX PS Claim 3; Page 20-22; 30pp; English.
XX XX The 37 kDa lactate dehydrogenase (LDH) (AAW11476) of Eimeria acervulina
XX CC schizonts, or immunologically active portions of it, can be used for
XX CC prodn. of vaccines against coccidiosis in poultry. The LDH can be
XX CC isolated from schizonts or produced in host cells or organisms
XX CC transformed with recombinant vectors including LDH nucleic acids (see
XX CC also AAT51370). Live viral vaccines can also be produced. (Updated on 17-
XX OCT-2003 to standardise OS field)

SQ Sequence 330 AA;

Query Match 99.8%; Score 1685; DB 2; Length 330;
Best Local Similarity 99.7%; Pred. No. 1.5e-158;

applicant

Matches 329; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVFEKTRPKIAMVSGMIGTGMFLCSLRELGDVVLFDVVPNPMGKAMDISHNSSVV 60
DB 1 MAVFEKTRPKIAMVSGMIGTGMFLCSLRELGDVVLFDVVPNPMGKAMDISHNSSVV 60

QY 61 DTGITVYGSNYSYELCKGADVVIITAGITKIPGSKDKESRMDLLPVNIKIMRDVGAIAKS 120
DB 61 DTGITVYGSNYSYELCKGADVVIITAGITKIPGSKDKESRMDLLPVNIKIMRDVGAIAKS 120

QY 121 YCPNFAVINITNPLDVNVAALQSSGLPHHRICGMAGLQSSRFRMRIMADKLEVSFPRDVQ 180
DB 121 YCPNFAVINITNPLDVNVAALQSSGLPHHRICGMAGLQSSRFRMRIMADKLEVSFPRDVQ 180

QY 181 GMWIGVGHDMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIIVQKTKVAGGEIVRLLGQG 240
DB 181 GMWIGVGHDMVPLSRVATVNGIPLSEFVKKGWIKQEEVDIIVQKTKVAGGEIVRLLGQG 240

QY 241 SAYYAPGASAIQMAESYLKDKRVMVCSYLOGQYGVQNHLYGVPCVIGRGVEKIELE 300
DB 241 SAYYAPGASAIQMAESYLKDKRVMVCSYLOGQYGVQNHLYGVPCVIGRGVEKIELE 300

QY 301 LTAQEROELQSGIDEVKEMOKAIAALDASK 330
DB 301 LTAQEROELQSGIDEVKEMOKAIAALDASK 330

RESULT 2
ID ADS28805 standard; protein; 320 AA.

AC ADS28805;
DT 02-DEC-2004 (first entry)
DE Bacterial polypeptide #17838.

Recombinant DNA construct; transformed plant; improved plant property;
cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbohydrate;
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polypeptide.

Bacteria.

US2003233675-A1.

18-DEC-2003.

20-FEB-2003; 2003US-00369493.

21-FEB-2002; 2002US-0360039P.

(CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 17838; 122pp; English.

The invention relates to a recombinant DNA construct comprising a
promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX
SQ Sequence 320 AA;

Query Match 52.2%; Score 880.5; DB 8; Length 320;
Best Local Similarity 53.9%; Pred. No. 1.6e-78;
Matches 173; Conservative 54; Mismatches 89; Indels 5; Gaps 1;

QY 9 RPKIAMVSGMIGTGMFLCSLRELGDVVLFDVVPNPMGKAMDISHNSSVVDTGITVYG 68
DB 3 RKKIALIGSGMIGTGLAHLAAIKELGDIVLFDIAEGTPOGKALDIQAQSGPVEGFDANLKG 62

QY 69 SNSYECLKGADVVIITAGITKIPGSKDKESRMDLLPVNIKIMRVGAIAKSCPNAFVI 128
DB 63 ANSYEDIAGADVCIIVTAGIPRKEG-----MSRDDLKTNLGVMAKVGEGIAAHAPDAFVI 117

QY 129 NITNPLDVNVAALQSSGLPHHRICGMAGLQSSRFRMRIMADKLEVSFPRDVQWIGVHG 188
DB 118 CITNPLDVNVAALQSSGLPHHRICGMAGLQSSRFRMRIMADKLEVSFPRDVQWIGVHG 177

QY 189 DHMVPILSRVATVNGIPLSEFVKKGWIKQEEVDIIVQKTKVAGGEIVRLLGQSAIYAPGA 248
DB 178 DTMPVIEYSTVAGIPVPLIKMGWSTQERIDAIIVARTSGGGEIVALLKTGSAYYAPAT 237

QY 249 SAIQMAESYLKDKRVMVCSYLOGQYGVQNHLYGVPCVIGRGVEKIELELTAQEROE 308
DB 238 SAIQMAESYLKDKRVMVCSYLOGQYGVQNHLYGVPCVIGRGVEKIELELTAQEROE 297

QY 309 LOGSDEVKEMOKAIAALDAS 329

DB 298 FDSVDVAVKELVAACKSIDAS 318

RESULT 3

ADS22408

ID ADS22408 standard; protein; 319 AA.

XX

AC ADS22408;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #11441.

Recombinant DNA construct; transformed plant; improved plant property;
cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbohydrate;
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polypeptide.
Bacteria.

CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 322 AA;

Query Match 51.1%; Score 862; DB 8; Length 322;
 Best Local Similarity 53.3%; Pred. No. 1.1e-76;
 Matches 174; Conservative 56; Mismatches 87; Indels 8; Gaps 2;
 QY 9 RPKIAMVSGMIGGTMAFLCSRLRELDGVVLFDPVPMMPMGKAMDISHNSSVVDGTGTVYG 68
 DB 3 RNKIALIGSGMIGGTMAHMLGLKDLGDVLFDAEIGIPQKGLDIAQSPVDGFSRLTG 62
 QY 69 SNSYECLKGADVVIITAGITKIPGSKDKWSRMDLLPVNIMKIMREYGAIAKSYCPNAFVI 128
 DB 63 VNDYAGIEGADVCIIVTAGVPRKPG-----MSRDDLLGLNLMKVMQVQVGLKKYAPKAFVI 117
 QY 129 NITNPLDVMVAALQESSGLPHHRIICMGAGMLDSSRRFRMIADKLEVPSPDVQGMVGVHG 188
 DB 118 CITNPLDAMVWALQKESGLPKTHVVGAGVLSAREFYLAEEFKVSVSDVTAFLVGGHG 177
 QY 189 DHMVPPLSRVATVNGIPLSEFVKKGWIKQBEVDIVQTKVAGGEIVRLLGQGSAYYAPGA 248
 DB 178 DSMVPMIRVTSVGIPLDLVPMGWTSKELQIVQTRDGGAEIVGLLKTGSAYYAPAA 237
 QY 249 SAIQMAESYLKDKRRVMVCSYLGQYGVQNHVYLGPCVIGRGVGEIKIIELELTAQERQE 308
 DB 238 SAIAMAESYLKDKRRVLPCLAAHLSGQYGVKGTGVGVVVGAGGVVERIIEIDLKSEQKM 297
 QY 309 LQGSIDEVKEMQKA---IAALDASK 330
 DB 298 FESSVATVOGLTEACVKIAPQLASK 322

RESULT 8
 ADS28046
 ID ADS28046 standard; protein; 320 AA.

AC ADS28046;
 XX
 XX 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #17079.
 DE
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

OS Bacteria.
 XX
 XX US200233675-A1.
 PN
 XX 18-DEC-2003.
 XX
 XX 20-FEB-2003; 2003US-00369493.
 PF
 XX 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.

DR New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 17079; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX

SQ Sequence 320 AA;

Query Match 50.4%; Score 850.5; DB 8; Length 320;
 Best Local Similarity 51.1%; Pred. No. 1.6e-75;
 Matches 164; Conservative 60; Mismatches 92; Indels 5; Gaps 1;
 QY 9 RPKIAMVSGMIGGTMAFLCSRLRELDGVVLFDPVPMMPMGKAMDISHNSSVVDGTGTVYG 68
 DB 3 RAKIALIGAGMIGGTMAHIAAREELGDVILFDIAEGTPQKALDIAEASAVFGKDVALKG 62
 QY 69 SNSYECLKGADVVIITAGITKIPGSKDKWSRMDLLPVNIMKIMREYGAIAKSYCPNAFVI 128
 DB 63 ANDYADIAGADVCIIVTAGVPRKPG-----MSRDDLLGLNLMKVMKAVGEGIKAHAPNAFVI 117

QY 129 NITNPLDVMVAALQESSGLPHHRIICMGAGMLDSSRRFRMIADKLEVPSPDVQGMVGVHG 188
 DB 118 CITNPLDAMVWALQKESGLPKTHVVGAGVLSAREFYLAEEFKVSVSDVTAFLVGGHG 177
 QY 189 DHMVPPLSRVATVNGIPLSEFVKKGWIKQBEVDIVQTKVAGGEIVRLLGQGSAYYAPGA 248
 DB 178 DSMVPMIRVTSVGIPLDLVPMGWTSKELQIVQTRDGGAEIVGLLKTGSAYYAPAE 237
 QY 249 SAIQMAESYLKDKRRVMVCSYLGQYGVQNHVYLGPCVIGRGVGEIKIIELELTAQERQE 308
 DB 238 SAIAMAESYLKDKRRVLPCLAAHLSGQYGVKGTGVGVVVGAGGVVERIIEIDLKSEQKM 297
 QY 309 LQGSIDEVKEMQKAIAALDAS 329
 DB 298 FAKSVESVGLMEACKAIDSS 318

RESULT 9
 ADN25360
 ID ADN25360 standard; protein; 320 AA.

XX AC ADN25360;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #8013.
XX DE
XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KW pathogen tolerance; pest tolerance; plant disease resistance;
XX KW cell cycle pathway modification; plant growth regulator;
XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KW bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.
XX PN 18-DEC-2003.
XX PF 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX DR WPI; 2004-061375/06.
XX XX New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 8013; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polypeptide used in the
XX CC scope of the invention. Note: The sequence data for this patent did not
XX CC form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 320 AA;
Query Match 50.3%; Score 848.5; DB 8; Length 320;
Best Local Similarity 50.8%; Pred. No. 2.5e-75;
Matches 163; Conservative 64; Mismatches 89; Indels 5; Gaps 1;
9 RPKIAMVGSIGCTTAFGLSLRELGLDVLFDVVPNNPMGKAMDISHSSVDTGITVYG 68

Db 3 RPKIALIGAGQIGTTLAHLAAIKELGDVWLFDAEFTPOQSKALDIAQSGSPSEGFDAVMKG 62
Qy 69 SNSYECLKGADVVIIITAGITKIPGKSDKWSRMDLLPVNIKIMREVGAALKSYCPNFAVI 128
Db 63 ANSYEEIAGADVCIIVTAGVPRKFG-----MSRDDLLIGINLKVMSVGEIGIKAHAPNAFI 117
Qy 129 NITNPDLVWVAALQESSGLPHHRIICMAGMLDSSRRFRMIADKLEVSPRDVQGMVIGVHG 188
Db 118 CITNPDLAMVWALQQFSGLPAEKVVMAGVLDARSFRHFLSVFNVMSRMDVTAFLVGGHG 177
Qy 189 DHMVPISRYATVNGIPLSEFVKKGWIKQOEVDIVOKTKVAGGEIVRLGQGSAYAPGA 248
Db 178 DTWVPLRVYSTVAGIPLPLVQMGWTTQEKLDIOIVORTDGGAEIVGLLTKTSAFAPAT 237
Qy 249 SAIQMAESYLKDRKRVWVSCYLGQGVGVONHYLGPVPCVIGRGVKEIIELELTAQBROE 308
Db 238 SALEMAEAYLKQKQKRLLPAAVYDGAFLNGVMYGVPTTIAGGIEKIVDKLNDDEQAM 297
Qy 309 LQGSIDEVEMQKAIALDAS 329
Db 298 FDKSVNAVGLVEACKGIDSS 318
RESULT 10
ADS21490
ID ADS21490 standard; protein; 320 AA.
AC ADS21490;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #10523.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KW pathogen tolerance; pest tolerance; plant disease resistance;
XX KW cell cycle pathway modification; plant growth regulator;
XX KW homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KW bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.
XX PN 18-DEC-2003.
XX PF 20-FEB-2003; 2003US-00369493.
XX PR 21-FEB-2002; 2002US-0360039P.
XX PA (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX DR WPI; 2004-061375/06.
XX XX New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 10523; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polypeptide used in the
XX CC scope of the invention. Note: The sequence data for this patent did not
XX CC form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 320 AA;

transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactonannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 320 AA;

Query Match 50.2%; Score 847.5; DB 8; Length 320;
Best Local Similarity 52.0%; Pred. No. 3.1e-75;
Matches 167; Conservative 61; Mismatches 88; Indels 5; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSLRELGDVVLFDVVPNMPKAMDISHNSVVDGTGITYVG 68
DB 3 RKXIALIGAGNIGTTLAHLAAQKELGDVILFDVVEGVPQKALDLSQCQPFVEGFDAIIG 62
QY 69 SNSYECLKGADVVIITAGITKIPGKSDKESRMDLLPVNIIKIMREVGAAIKSCPNAFVI 128
DB 63 TNDYKGIAGADVLIIVTAGVARKG-----MSRDDLLGINLKVNAKAGEGIRDNAPAFVI 117
QY 129 NITNPLDVVMAALQESSGLPHHRIICGMAGMLDSSRRFRMIADKLEVSPRDVQGMVIGVHG 188
DB 118 CITNPLDMVAWLRFSGLPANKVGVAGVLDARSFTFLAWFVGSIRDVNTFVLGGHG 177
QY 189 DHMVPFSRYATVNGIPLSEFVKKGWIKOEVDVIVOKTKVAGEIVRLILGQGSAYYAPGA 248
DB 178 DTWVPVTVSTVNGIIPVDLVKMGSLTQEKIDAIQVTRSGGGEIVGLLKTGSFAFYAPAA 237
QY 249 SAIQMAESVLDKRVKVMVSCYLGQGVQVNHVLPVCPVIGRGVGEKIIELELTAQERQE 308
DB 238 SGTMAEAYLNDKRLIPCAAYVDGYGVNGLVGVFVLIGANGVEKVEIELDDAKGN 297
QY 309 LQGSIDEVKEMQKAIALDAS 329
DB 298 LQVSDAVKLEACKGIDPS 318

RESULT 11
AAR62605
ID AAR62605 standard; protein; 315 AA.
AC AAR62605;
XX AAR62605;

DT 25-MAR-2003 (revised)
DT 18-JUL-1995 (first entry)

XX P. falciparum lactate dehydrogenase.

XX Lactate dehydrogenase; LDH; immunogen; antibody; immunisation; detection;
KW Plasma; serum; malaria.

XX Plasmodium falciparum.

XX WO9424287-A1.

XX 27-OCT-1994.

XX 06-APR-1994; 94WO-US003796.

PR 12-APR-1993; 93US-00046160.
XX (DART-) DARTMOUTH COLLEGE.
XX Bzik DJ, Fox BA;
XX WPI; 1994-341866/42.
DR N-PSDB; AAQ72947.
XX Isolated gene encoding lactate dehydrogenase of P. falciparum - and methods for diagnosis and vaccination against malaria.
PT Claim 5; Page 18-19; 35pp; English.
XX This sequence represents P. falciparum lactate dehydrogenase (LDH). The LDH protein and immunogenic fragments of it may be used as an immunogen for antibody generation. The progress of immunisation can be monitored by detection of antibody titres in plasma or serum. Antibodies raised against fragments of LDH can be used to immunise against P. falciparum infection and to detect early malarial infection. See also RR62606-14. (Updated on 25-MAR-2003 to correct PN field.)
CC SQ Sequence 315 AA;

Query Match 49.1%; Score 828; DB 2; Length 315;
Best Local Similarity 52.6%; Pred. No. 2.7e-73;
Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSLRELGDVVLFDVVPNMPKAMDISHNSVVDGTGITYVG 68
DB 4 KAKIVLVSIGMIGVMAFLIVQKILGDVVLFDVVPNMPKALDTSHTNMVAYSNCVSG 63
QY 69 SNSYECLKGADVVIITAGITKIPGKSDKESRMDLLPVNIIKIMREVGAAIKSCPNAFVI 128
DB 64 SNTYDLGADVVIIVTAGITKAPGKSDKESRMDLLPVNIIKIMREVGAAIKSCPNAFVI 123
QY 129 NITNPLDVVMAALQESSGLPHHRIICGMAGMLDSSRRFRMIADKLEVSPRDVQGMVIGVHG 188
DB 124 VTNPVDVWVQLLHSHGSGVPKNIILGLGVLDTSRLKYIISQKLVNCPDVNAHIVGANG 183
QY 189 DHMVPFSRYATVNGIPLSEFVKKGWIKOEVDVIVOKTKVAGEIVRLILGQGSAYYAPGA 248
DB 184 NKWLLKRYITVGGIPLQEFINNKLIISDAELEAIFDRTVNTALEIVNL--HASPYVAPAA 241
QY 249 SAIQMAESVLDKRVKVMVSCYLGQGVQVNHVLPVCPVIGRGVGEKIIELELTAQERQE 308
DB 242 AIIEMAESYLKDLKKVLCSTLLEGGYGHSDIFGFTPVVLGANGVEQVIELQINSEKAK 301
QY 309 LQGSIDEVKEMQ 320
DB 302 FDEAIAETKRMK 313

RESULT 12
AAY01690
ID AAY01690 standard; protein; 315 AA.
AC AAY01690;
XX AAY01690;

DT 23-JUN-1999 (first entry)

XX A Plasmodium falciparum lactate dehydrogenase.

XX Lactate dehydrogenase; LDH; antibody; antigenic peptide; malaria;
KW immunization; Plasmodium falciparum infection;

XX Plasmodium falciparum.

XX WO9913903-A1.

XX 25-MAR-1999.

XX 08-SEP-1998; 98WO-US018626.

XX 17-SEP-1997; 97US-00932194.
 XX (DART-) DARTMOUTH COLLEGE.
 XX Bzik DJ, Fox BA;
 XX WPI; 1999-229405/19.
 XX N-PSDB; AAX26909.
 XX New antibodies to Plasmodium falciparum.
 XX Claim 1; Page 36-37; 46pp; English.
 XX The present sequence represents a Plasmodium falciparum lactate
 CC dehydrogenase (LDH). The specification describes an antibody which binds
 CC to antigenic peptides derived from the LDH protein. The antibody can be
 CC used for diagnosing or treating malaria in a subject. The peptides and
 CC portions can be used for immunizing an individual against malaria and the
 CC antibody can also be used for diagnosing Plasmodium falciparum infections
 XX
 XX SQ Sequence 315 AA;
 Query Match 49.1%; Score 828; DB 2; Length 315;
 Best Local Similarity 52.6%; Pred. No. 2.7e-73;
 Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;
 QY 9 RPKIAMVSGMIGTMAFLCSRLRELGVDVLFVVPNNPMGKAMDISHNSSVVDITGVYG 68
 DB 4 KAKIVLVSIGMIGVGMATLIVQKNLGDVLFVVPNNPMGKALDTSHTNWMAYSNCKVSG 63
 QY 69 SNSVECLKGDADVITITAGITKIPGSKDSESRMDLLPVNLIKIMREVGAAIKSYCPNAPVI 128
 DB 64 SNTYDDLAGADVITVITAGFTKAPGSKDSESRMDLLPVNLIKIMREVGAAIKSYCPNAPVI 123
 QY 129 NITNPLDMVNAALQESSGLPHRICGWSRMDLLPVNLIKIMREVGAAIKSYCPNAPVI 198
 DB 124 VTNFVDMVQVLLHQSFGVKNKILGGVLDTSRLKYISQKLNVCPRDVAHIVGAHG 183
 QY 189 DHMVPISRYATVNGIPLSEFVKGWIKQEEVDIVQKTVAGGIVRLGGGSAAYAPGA 248
 DB 184 NKWVLLKRYITVGGIPLOEFINNNKLSIDAEALFDFVTVALEIVNL--HAPFYVAPAA 241
 QY 249 SAIQMAESYLKDRKRVNVCSCYLGQYGVQVNHVLPVPCVIGRGVEKIELELTAQERQE 308
 DB 242 AIEMAESYLKDLKKVLCISLLEGGYGHSDIFGGTPVWLGANGVEQVIELQNLSEBKA 301
 QY 309 LQSSIDEVKEMQ 320
 DB 302 FDEAIAETKRMK 313
 RESULT 13
 ADS44807
 ID ADS44807 standard; protein; 312 AA.
 XX ADS44807;
 AC ADS44807;
 XX 02-DEC-2004 (first entry)
 DT Bacterial polypeptide #23237.
 DE
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS
 XX
 PN US2003233675-A1.

XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI WPI; 2004-061375/06.
 DR New recombinant DNA construct comprising a promoter positioned to provide
 XX for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 23237; 122pp; English.
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX SQ Sequence 312 AA;
 Query Match 43.8%; Score 740; DB 8; Length 312;
 Best Local Similarity 45.9%; Pred. No. 1.5e-64;
 Matches 147; Conservative 63; Mismatches 98; Indels 12; Gaps 3;
 QY 7 NTRPKIAMVSGMIGTMAFLCSRLRELGVDVLFV--VPMNPMGKAMDISHNSSVVDITGI 64
 DB 3 NTRKKSIVGAGTGTATTATLQAKELADVLDVLDIPOLENPTKGLDMLSEASPVQGFDA 62
 QY 65 TVYGSNSYECLKGDADVITITAGITKIPGSKDSESRMDLLPVNLIKIMREVGAAIKSYCPN 124
 DB 63 KITGTSNYEDTAGSDIWIITAGIARKPG-----MSRDDLVSTNEKIMRSVTQIEVKYSPD 117
 QY 125 AFVINITNPLDMVNAALQESSGLPHRICGWSRMDLLPVNLIKIMREVGAAIKSYCPN 184
 DB 118 SIIVLITNPVDANTYAVYKESGPGKERVIGSQGVLDTRFTFAEELNLSKVDVTGFLV 177
 QY 185 GVHGDHWPVLSRYATVNGIPLSEFVKGWIKQEEVDIVQKTVAGGIVRLGGGSAAY 244
 DB 178 GGHGDDWVPLVRSYAGGIPLETLPK-----BRIDAIVERTRKGGGIVNLLGNSAY 232
 QY 245 APCASAIQMAESYLKDRKRVNVCSCYLGQYGVQVNHVLPVPCVIGRGVEKIELELTAQ 304
 DB 233 APAASLTEMVEAILKQRRVLPITAYLEGEYEGYILGVPTIVGNGLEQIELELTDY 292

QY 305 EROBLOGSIDEVEMOKAIA 324
DB 293 ERAQLNKSVESVKNVMKVL 312

RESULT 14
ID ADS28362 standard; protein; 314 AA.
AC ADS28362;
XX 02-DEC-2004 (first entry)
DE Bacterial polypeptide #17395.

XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.

XX Bacteria.
XX US2003233675-A1.
XX 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 17395; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic

CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 314 AA;
SQ Query Match 42.0%; Score 709; DB 8; Length 314;
Best Local Similarity 44.0%; Pred. No. 1.8e-61;
Matches 140; Conservative 67; Mismatches 97; Indels 14; Gaps 4;

QY 9 RPKIAMVSGMIGCTMAFLCSLRELGDDVVLFDVPMNM---PMCKAMDISHNSSVVDGTG 65
DB 5 RRVSVVIGAGFTGATTALMVAQKELGDLVLD-IPQMEGFTKGKALDMLLESTPVQGVQDVN 63
QY 66 VYGSNSYECLKGADVVITAGITKIPGKSDKEWSRMDLLPVNIKIMREYGAIAIKSYCPNA 125
DB 64 ITGTSSEYTKDSDDVVITAGIARKEG-----MSRDDLVSTNAGIMKATVKEVVKHSPNA 118
QY 126 FVINITNPLDVMAALQESSGLPHHRICGMAGMLSSRRPRMIADKLEVPSPRDVQGMVIG 185
DB 119 YIIULTNPADAMTYTVYKESGFPKRVIGSQSVGLDTARFRTFVAQELNLSVEDITGFLVG 178
QY 186 VHGDDHVPPLSRVATVNGIPLSEFVKKGWIKQEVDDIVOKTKVAGGEIVRLLLGGSAYYA 245
DB 179 GHGDDMVPLIRYSYAGGIPLEKL-----LPQRIIDAIVERTRKGGEIVGLLNGSAYYA 233
QY 246 PGASAIQMAESYLKDKRVMVCYLOGQYQNNHYLGVPCVIGRGVKEIIELELTAOE 305
DB 234 PAASLAEMVEAILKDKRVLPFTIAYLEGEYGEDIVGVPTILGGDGIKFIELDLTDEE 293
QY 306 ROELOGSIDEVEMOKAI 323
DB 294 KATFAKSIESVRNMSAL 311

RESULT 15
AAR94013
ID AAR94013 standard; protein; 329 AA.
XX AAR94013;
XX 16-OCT-2003 (revised)
DT 21-AUG-1996 (first entry)
XX Heat resistant maleate dehydrogenase.
DE Heat resistant maleate dehydrogenase.
KW Heat resistant maleate dehydrogenase; h-rPAD; NADH; L-aspartic acid;
KW alpha-ketoglutaric acid; glutamine oxalo-transaminase activity; GOT.
XX Geobacillus stearothermophilus; ATCC 12016.

XX Key Location/Qualifiers
FT Misc-difference 185 /note= "Given in the specification as Var"
XX JP08047389-A.
XX 20-FEB-1996.
XX 01-JUL-1994; 94JP-00151045.
XX 02-JUL-1993; 93JP-00164701.
PR 03-JUN-1994; 94JP-00121629.
XX (TOYM) TOYOBO KK.
PA WPI; 1996-166248/17.
XX N-PSDB; AAT17715.
DR Protein having heat resistant malate dehydrogenase activity - and reagent
PT conlg. protein, NADH and L-aspartic and alpha-keto-glutaric acid for
PT determination of glutamine oxalo-transaminase activity.
XX Claim 8; Page 13-15; 17pp; Japanese.

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